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Result
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                M. catarrhalis BAS
Moraxella catarrha
M. catarrhalis BAS
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     Novel human diagno
                     Drosophila melanog
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screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic components of arrays which are useful to produce antibodies, and as a purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists antagonists are bacteristatic) are used for the treatment and prevention of which are bacteristatic) are used for the treatment and prevention of diseases including bacterial infection, otitis media in infants and
                                                                                                                  This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for
                                                                                                                                                                                 Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                           Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                   N-PSDB; AAZ40351.
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                                                                          Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
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This sequence is a Moraxella catarrhalis BASB019 protein of the

Claim 3; Fig 3; 101pp; English

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WPI; 2000-062148/05
                                                                                                                                                                                                                                                                                                                                                                                                                                  BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention;
                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                          03-MAY-1999;
                                                                                                                                                                                                                                                                                   11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   upper respiratory tract infection; middle ear infection; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. catarrhalis BASB019 protein sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                        Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY55091 standard; Protein; 172 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREVNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LPSLVYFDEDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                              98GB-0009683
                                                                                                                                                                                                                    99WO-EP03038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.2%; Score 107; DB 21; Length 172; 100.0%; Pred. No. 4.4e-93; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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AAY55092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC identification, identification of mutation in BASB013 sequences, and as CC purposes. The polypeptides can be used to produce antibodies, and as a CC also be used in vaccine formulations, and to identify agonists and CC antagonists. The polypeptides, antibodies, agonists and antipolypeptides antibodies, and an according to the treatment and prevention of CC antagonists. The polypeptides, antibodies, agonists and antagonists and CC diseases including bacterial infection, other treatment and prevention of CC children, pneumonia in the elderly sinusitis, noscomial infections and CC invasive diseases, chronic otitis media with hearing loss, fluid CC invasive diseases, chronic otitis media with hearing loss, fluid CC invasive diseases, chronic otitis media with hearing loss, fluid CC infection. They are also used in the prevention of adhesion of bacteria CC infection. They are also used in the prevention of adhesion of bacteria CC extravolic matrix proteins on in-dwelling devices, or to extracellular CC proteins on wounds, and to thus prevent tissue damage and/or block the control of the upper respiratory tract and middle ear contain progression of pathogenesis in infections initiated other than by CC The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M catarrhalis affections has risen dramatically,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
       03-MAY-1999;
                                                                                                                                                      BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                    11-NOV-1999.
                                                                                               W09957277-A2
                                                                                                                                     Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                  M. catarrhalis BASB019 protein sequence #4.
                                                                                                                                                                                                                                                                                                                                                              01-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                AAY55092;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY55092 standard; Protein; 172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and it is no longer common to isolate M. catarrhalis strains that are resistant to standard antibiotics. The BASB019 products of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hypridisation probes, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 3; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening of genetic mutations, serotype, organism or strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREVNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 AA;
                                                                                                                                                                                                                                                                                                                                                         (first entry)
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99WO-EP03038.
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identification, identification of mutation in BASBO13 sequences, and as cc components of arrays which are useful for diagnostic and prognostic c purposes. The polypeptides can be used to produce antibodies, and as a cc purposes. The polypeptides can be used to produce antibodies, and as a cc also be used in vaccine formulations, and to identify agonists and cc antagonists. The polypeptides, antibodies, agonists and antagonists and cc antipodies, including bacterial infection, otilis media in infants and cc (which are bacteristatic) are used for the treatment and prevention of cc diseases including bacterial infection, otilis media in infants and cc diseases including bacterial infection, otilis media in infants and cc children, pneumonia in the elderly, sinusitis, nosocomial infections and cc invasive diseases, chronic otilis media with hearing loss, fluid cc infection in the middle ear, auditive nerve damage, delayed speech accumulation in the middle ear, auditive nerve damage, of the extracellular cc infection. They are also used in the prevention of adhesion of bacteria cc infection of mounds, and to thus prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the cc proteins on wounds, and to thus prevent tissue damage and/or block the proteins on for adversing the surfacellular cc the implantation of in-dwelling devices or by other surgical techniques. The implantation of pathogenesis in infections has risen dramatically, created to standard antibiotics. The BASBO19 products of the invention cc resistant to standard antibiotics. The BASBO19 products of the invention content in the common to isolate M. catarrhals strains that are
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       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-062148/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for polynucleotides may be used as a source for hybridisation probes, and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening of genetic mutations, serotype, organism or strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistant bacteria
BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                                                                                                                                                                               AAY55093 standard; Protein; 16 AA.
                                                                                                                                                 M. catarrhalis BASB019 protein sequence fragment.
                                                                                                                                                                                                    01-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                            126 VAVRNYLL 133
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; Pred. No. 3.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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This sequence is a fragment of a Moraxella catarrhalis BASHO19 protein of CC the invention. The sequences can be used for diagnosis of disease, conditions of disease, or determining response of an infectious organism to CC staging of disease, or determining response of an infectious organism to CC grobes, and for screening of genetic mutations, serotype, organism or CC probes, and for screening of genetic mutations, serotype, organism or CC grant and for screening of genetic mutations, serotype, organism or CC strain identification, identification of mutations, sequences, CC strain identification, identification for diagnostic and CC grognostic purposes. The polypeptides can be used to produce antibodies, CC prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The CC and as a target for the screening of antimicrobial drugs. The polypeptides and antagonists and antagonists. The polypeptides, antibodies, agonists and cCC antagonists (which are bacteristatic) are used for the treatment and CCC antagonists (which are bacteristatic) are used for the treatment and CCC infants and children maximum and in the olderly simulations, otitis media in greening of antipolic antipolic and antagonists and antagonists and antagonists and antagonists and antagonists and antagonists. The polypeptides, antibodies, agonists and antagonists and antagonists and antagonists and antagonists. The polypeptides antibodies, agonists and antagonists and antagonists and antagonists and antagonists and antagonists and antagonists. The polypeptides, antibodies, agonists and antagonists and a
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AAY57577
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       KW XXX ACX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 speech learning, infection of the upper respiratory tract and middle ear speech learning, infection of the upper respiratory tract and middle ear infection. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular to eukaryotic matrix proteins on in-dwelling devices or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on by other surgical techniques, the implantation of in-dwelling devices or by other surgical techniques, the implantation of in-dwelling devices or by other surgical techniques, the implantation of in-dwelling devices or by other surgical techniques and it is no longer common to isolate M. catarrhalis strains that are and it is no longer common to isolate M. catarrhalis strains that are and it is no longer common to isolate M. catarrhalis strains that are can be used screen for new antibacterial compounds that may target these can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infants and children, pneumonia in the elderly, sinusitis, nosocomial infants and children, pneumonia in the elderly, sinusitis, nosocomial infections and invasive diseases, chronic otitis media with hearing loss, infections and invasive diseases, auditive nerve damage, delayed fluid accumulation in the middle ear, auditive nerve damage, delayed
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                                                                                                                                                                                                                                                                                                             AAY57577 standard; peptide; 16 AA.
                                                                                                     Moraxella catarrhalis BASB020 specific peptide SEQ ID NO:13.
otitis media; pneumonia; sinusitis; anti-inflammatory; auditory;
                                    Moraxella catarrhalis; BASB020; diagnosis; vaccine; infection;
                                                                                                                                                                          02-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 NEEAWSQNRRAELSY 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NEEAWSQNRRAELSY 16
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100.0%; Pred. No. 4.8e-07
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RESULT 7
AAY55094
ID AAY55
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AAC AAY5
XX
AC AAY5
XX
DT 01-P
DT 01-P
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BASI
KW BASI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collules of Ollies General Series and polypoptides are used as research CC reagents and materials for discovery of treatments of and diagnostics for CC human diseases. Probes comprising BASBO20 nucleotide sequences can be constructed to conduct efficient screening of genetic mutations, CC serotype, taxonomic classification or identification. The polynucleotide compounds. The polypeptides and polynucleotides are used to block the CC initial physical interaction between a gram negative and/or gram positive bacteria to the mammalian host. The polynucleotides encoding certain CC bacteria to the mammalian host. The polynucleotides encoding certain CC mon variable regions of bacterial cell surface protein are used in CC experiments in animal models of infection with M.catarrhalis to conditify protein apitopes able to provoke a prophylactic or therapeutic composition comprising an antibody CC directed against BASBO20 can be used for treating humans with moscomial M. catarrhalis diseases such as sinusitis, otitis media and nosocomial
                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; immune response; immunisation; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a peptide specific for a BASB020 protein, isolated from Moraxella catarrhalis, used in an example from the present invention. BASB020 polynucleotide fragments may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-062301/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9958684-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNAs and genomic clones encoding BASB020 and to isolate cDNA and clones of other genes that have high sequence identity to BASB020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hybridisation probes for RNA, cDNA and genomic DNA to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 69; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        otitis media, pneumonia, sinusitis etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptides useful as vaccines for Moraxella infections such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thonnard J;
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               BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection;
                                                                                                                                                                     AAY55094;
                                                                                                                                                                                                        AAY55094 standard; Protein; 14 AA.
                                                                                           M. catarrhalis BASB019 protein sequence fragment.
                                                                                                                                  01-MAR-2000
 invasive disease; delayed speech learning;
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                      158 NEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-0010285
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                                                                                                                                                                                                                                                                                                                                                                                          8.7%;
                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                          Score 15;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            DB 21; 1
                                                                                                                                                                                                                                                                                                                                                                                                              Length 16;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 8
AAY57578
XXX DXX ACX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and can also have bacteristatic) are used for the treatment and prevention of diseases including bacterial infection, othits media in cc infections and invasive diseases, chronic otitis media with hearing loss, clid accumulation in the middle ear, auditive nerve damage, delayed cc speech learning, infection of the upper respiratory tract and middle ear confection. They are also used in the prevention of adhesion of bacteria cc infections on wounds, and to thus prevent tissue damage and/or block the cormal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or to extracellular cc the implantation of pathogenesis in infections initiated other than by the implantation of pathogenesis in infections initiated other than by created the implantation of pathogenesis in infections has risen dramatically. The frequency of Moraxella catarrhalis infections has risen dramatically, can be used in the prevent the BASBO19 products of the invention created and to standard antibiotics. The BASBO19 products of the invention catarrhalis strains that are
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antinicrobial drugs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a fragment of a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Page 70; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel BASB019 polynucleotides and polypeptides from Moraxella
                                  Moraxella catarrhalis BASB020 specific peptide SEQ ID NO:14.
                                                                                02-MAR-2000
                                                                                                                          AAY57578;
                                                                                                                                                                 AAY57578 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistant bacteria
                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
                                                                                                                                                                                                                                                                                                             46 YTGVAPLVDNDETV 59
                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                        1 YTGVAPLVDNDETV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                        14
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                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                             8.1%;
                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                             Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
. 3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 14;
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Moraxella catarrhalis; BASB020; diagnosis; vaccine; infection

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RESULT 9
                                                                                                                                                                                                                                ABB64563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a peptide specific for a BASB020 CC protein, isolated from Moraxella catarrhalis, used in an example from CC the present invention. BASB020 polynucleotide fragments may be used as CC hybridisation probes for RNA. CDNA and genomic DNA to isolate full-length CC clones and genomic clones encoding BASB020 and to isolate cDNA and genomic Clones of other genes that have high sequence identity to BASB020 gene. CC reagents and materials for discovery of treatments of and diagnostics for CC clones of other genes that have high sequences of an diagnostics for CC constructed to conduct efficient screening of genetic mutations. CC sequences can be used in the discovery of genetic mutations. CC sequences can be used in the discovery and development of antibacterial compounds. The polypeptides and polynucleotides are used to block the initial physical interaction between a gram negative and/or gram positive bacteria to the mammalian host. The polynucleotides encoding certain cc unariable regions of bacterial cell surface protein are used in CC polynucleotide constructs which are useful for genetic immunisation CC experiments in animal models of infection with M.catarrhalis to cidentify protein epitopes able to provoke a prophylatetic or therapeutic commune response. A therapeutic composition comprising an antibody CC directed against BASB020 can be used for treating humans with
                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 20481.
                                                                                                                              26-MAR-2002
                                                                                                                                                                       ABB64563;
                                                                                                                                                                                                      ABB64563 standard; Protein; 2168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        otitis media; pneumonia; sinusitis; anti-inflammatory; auditory; antibacterial; immune response; immunisation; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                        Tocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catarrhalis diseases such as sinusitis, otitis media and nosocomial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-062301/05
                                                                                                                                                                                                                                                                                                                                             46 YTGVAPLVDNDETV 59
                                                                                                                                                                                                                                                                                                        1 YTGVAPLVDNDETV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptides useful as vaccines for Moraxella infections such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    media, pneumonia, sinusitis etc.,
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98GB-0010285
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                                                                                                                                                                                                                                                                                                                                                                                                    8.1%; Score 14;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
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                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 10
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                                                       31-MAR-2000;
23-AUG-2000;
                  (HYSE-) HYSEQ INC
                                                                                                                                                       11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                WO200175067-A2
                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #22187.
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic
                                                                                                                                                                                                                                                                                                                                                                                                                ABG22196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG22196 standard; Protein; 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 20481; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL08666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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mes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   979 AAAAAALSV 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AAAAAALSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2168 AA;
                                                       2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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Pred. No.
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18;
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22;

The invention

18

and

0; Indels Length 2168;

0; Gaps

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forensic;

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RESULT 11
AAG18977
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CC Note: The sequence data for this patent did not appear in the printed considered in the printed considered in electronic format directly from WIPO at the format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 8
       25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                    25-FEB-2000; 2000EP-0301439.
                                                                                                                                   EP1033405-A2
                                                                                                                                                      Zea mays subsp. mays.
                                                                                                                                                                                                                                            17-OCT-2000 (first entry)
                                                                                                                                                                            termination sequence;
                                                                                                                                                                                                                      Zea mays protein fragment SEQ ID NO: 20601.
                                                                                                                                                                                                                                                                                         AAG18977 standard; Protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                  ||||||||
|14 AAAAAALS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; SEQ ID No 52555; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                         8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           139 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
               99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                       Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 139;
). 14;
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                         0;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1999;
                                                                                                                      99US-0139899.
99US-0140353.
99US-0140354.
99US-0140695.
99US-0140823.
99US-0141287.
99US-0141287.
99US-0141287.
                                                                                                                                                                                                                        99US-0139750.
99US-0139763.
99US-0139817.
                                                                                                                                                                                                                                                         9908-0139452
9908-0139453
9908-0139454
9908-0139454
9908-0139456
9908-0139457
9908-0139457
9908-0139459
9908-0139459
9908-0139463
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99US-0136021.
99US-0136392.
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99US-0128234.
99US-0128714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0134941
99US-0135124
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19-JUL-1999
19-JUL-1999
19-JUL-1999
19-JUL-1999
20-JUL-1999
20-JUL-1999
20-JUL-1999
21-JUL-1999
21-JUL-1999
21-JUL-1999
22-JUL-1999
22-JUL-1999
22-JUL-1999
22-JUL-1999
23-JUL-1999

99US-0145085. 99US-0145087. 99US-0145089. 99US-0145192. 99US-0145145. 99US-0145218.

990S-0144331 990S-0144332 990S-0144333 990S-0144334 990S-0144352 990S-0144632 990S-0144814 990S-0144814 990S-0144814 990S-0145086

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RESULT 12
ABB62221
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В
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999
22-OCT-1999
25-OCT-1999
25-OCT-1999
26-OCT-1999
26-OCT-1999
26-OCT-1999
26-OCT-1999
28-OCT-1999
28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-0CT-1999;
14-0CT-1999;
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13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-1999;
21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1999;
                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 13455.
                                                                                                                                                                                                                                                                                                    ABB62221;
                                                                                                                                                                                                                                                                                                                       ABB62221 standard; Protein; 306 AA.
       {\rm New} isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions –
                                               WPI; 2001-656860/75.
N-PSDB; ABL06324.
                                                                                                                    23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                              Venter JC, Adams M,
                                                                                                                                                  23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                      27-SEP-2001.
                                                                                               (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                         27 AAAAAALS
                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 8; DB 2 ilarity 100.0%; Pred. No. 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0159293.
99US-0159294.
99US-0159295.
99US-0159330.
99US-0159331.
99US-0159637.
99US-0159637.
99US-0160761.
99US-0160776.
99US-0160814.
99US-0160814.
99US-0160814.
99US-0160815.
99US-0160815.
99US-0160815.
99US-0160815.
99US-0160815.
99US-0161360.
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Pred. No. 15;
                                                                               Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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27-JUL-1999;
28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
09-AUG-1999;

99US-0145224. 99US-0145276. 99US-0145913. 99US-0145918. 99US-0145919. 99US-0145951.

99US-0146386.
99US-0146388
99US-0147038.
99US-01477038.
99US-0147703.
99US-0147192.
99US-0147192.
99US-0147193.
99US-0147416.
99US-0147416.
99US-0147416.
99US-0147418.
99US-0147418.
99US-0147418.

110-AUG-1999;
111-AUG-1999;
122-AUG-1999;
13-AUG-1999;
15-AUG-1999;
16-AUG-1999;
17-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
24-AUG-1999;
27-AUG-1999;
28-EEP-1999;
29-EEP-1999;
21-EEP-1999;
21-EEP-1999;
22-EEP-1999;
23-EEP-1999;
24-EEP-1999;
24-EEP-1999;
25-EEP-1999;
26-CGT-1999;
27-CGT-1999;
28-CGT-1999;
29-CGT-1999;
20-CGT-1999;
212-CCT-1999;
213-CCT-1999;
213-CCT-1999;
214-CCT-1999;
215-CCT-1999;
216-CCT-1999;
217-CCT-1999;

99US-0148684 99US-0149176 99US-0149723 99US-0149723 99US-0149923 99US-0150864 99US-0150866 99US-0151086 99US-0151086 99US-0151086 99US-0151086 99US-0151086 99US-0151086 99US-0151086 99US-0151086 99US-015108 99US-0151303 99US-01513363 99US-0154018 99US-0154018 99US-0154018 99US-0154018 99US-0155486 99US-0155486

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
              polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement (II) and its binding partners.
                                                                                                                                          The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                            Claim 20; SEQ ID No 41443; 103pp; English
                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                biodiversity
                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; food supplement; medical imaging; diagno;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and checkling cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #11075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG11084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG11084 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 13455; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed
             food supplement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POCGI
                                                                                                                                                                                                                                                                                           2001-639362/73.
DB; AAS75271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 IAAAAAAL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 IAAAAAAL 14
                                                                                                                                                                                                                                                                                                                                         RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
\widetilde{(	ext{II})} and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.7%; Score 8; 1
.00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                j; gene mapping; gene therapy; forensic;
imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                     Claim 2; Page 267; 1453pp; English.
                                                                                     Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                       Petersen J,
Tettelin H,
                                                                                                                                                                               Fraser C,
                                                                                                                     N-PSDB; AAZ53150
                                                                                                                                                                                                                                                                                                                01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and animo acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                      (GENO-)
                                                                                                                                                                                                                                                      09-OCT-1998;
                                                                                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                                                             09-OCT-1998;
                                                                                                                                                                                                                                                                                        02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                    30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 W09957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY74388 standard; Protein; 452 AA
                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigenic; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY74388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                              2000-062150/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AAAAAALS
                                                                                                                                                                                                  INST GENOMIC RES.
                                                                                                                                                                                                                   CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AAAAAALS 15
                                                                               and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitidis ORF 081 protein sequence SEQ ID NO:252.
                                                                                                                                                                            Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 AA;
                                                                                                                                                     Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                    Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                          98US-0099062.
98US-0103749.
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy.
                                                                                                                                                                                                                                       99US-0121528
                                                                                                                                                                                                                                                   98US-0103794
98US-0103796
                                                                                                                                                                                                                                                                                                  98US-0098994
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98US-0094869
                                                                                                                                                                                                                                                                                                                                                  99WO-US09346
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                                                                                                                                                                Grandi G,
Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8;
Pred. No.
                                                                                                                                                                Hickey
Ratti
                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; meningitis;
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                                                                                                                                                                ំ ដ
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                                                                                                                                                             Masignani V,
Scalato E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                            Mora M;
Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       septicaemia;
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0;

AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The

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RESULT 15
ABB58578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 2526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB58578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB58578 standard; Protein; 545 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2
                                                                                              discloses genomic DNA sequences (ABL16176-ABL30511), essequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                           useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                       Disclosure; SEQ ID NO 2526; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL02681.
                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila.
                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
Sequence
                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                               (ABB57737-ABB72072)
                             itp.wipo.int/pub/published_pct_sequences.
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    545 AA;
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2000US-0614150.
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o. 39;
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Query Match

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                                  AAU75084
                                                RESULT 17
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                                                                                                                                                                   Query Match
                                                                                                                                            Matches
                                                                                                                                                         Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB67264;
                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 28584; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                sequences (ABL01840
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                       genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
AAU75084;
                       AAU75084 standard; Protein; 606
                                                                                                                                                                                                                                                                                                                                                                                                            interactions
                                                                                                                                                        Local Similarity
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                                                                                       AAAAALS
                                                                                                                                                                                                 545 AA;
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                                                                                                                                              Conservative
                                                                                                                                                        4.7%; Score 8;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
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                                                                                                                                                                                                                                                                              isolated regulatory element from the nucleic acid sequences and a plant cell or seed transformed with the nucleic acid. An isolated regulatory element from these nucleotide molecules is useful for expressing an exogenous gene in plant cells. The nucleotide sequences of the invention and vectors containing these sequences are useful for expressing an plast and are useful as a molecular genetic marker for gualitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, in forage and turf grass improvement, e.g. tagging QTLs for dry matter digestibility, herbage quality, regrowth after cutting and grazing, cold tolerance, tiller survival and plant persistence. The present sequence represents the perennial ryegrass 4-coumarate Co-A-ligase 1 (LP4CL1) protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention represents purified or isolated nucleic acid and protein sequences of enzymes involved in lignin biosynthesis. The enzymes of the invention are 4 coumarate CoA-ligase (4CL), cinnamoyl-CoA reductase (CCR) and cinnamyl alcohol dehydrogenase (CDA) from a ryegrass (Lolium sp.) or fescue (Festuca sp.). The invention also comprises an invention are constructed to the construction of the comprises and comprises and comprise construction of the comprise construction of
                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid encoding enzymes involved in lignin biosynthetic pathway from ryegrass or fescue species useful for modifying lignin biosynthesis in plants and as a molecular genetic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perennial ryegrass; lignin; 4 commarate CoA-ligase; QTL; lignin biosynthesis; enzyme; cinnamoyl-CoA reductase; CCR; cinnamyl alcohol dehydrogenase; CAD; molecular genetic marker; qualitative trait loci; tagging; QTL mapping; DNA fingerprinting; marker assisted selection; forage improvement; turf grass improvement; dry matter digestibility; herbage quality; palatability; regrowth; cold tolerance; drought tolerance; tiller survival; plant persistence.
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                                                                                                                                                 Local
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13 QIAAAAAA 20
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                                                                                                                                              Similarity
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                                                                                                                                                                                                                                   .606 AA;
                                                                                                                Conservative
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                                                                                                                                        100.08;
                                                                                                                                     4.7%; Score 8; 1
100.0%; Pred. No.
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                                                                                                                                        DB 23;
o. 51;
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RESULT 19
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Best Local :
Drosophila; developmental biology; cell signalling; insecticide;
                             Drosophila melanogaster polypeptide SEQ ID NO 27429.
                                                           26-MAR-2002
                                                                                       ABB66879;
                                                                                                           ABB66879 standard; Protein; 637
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                               useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 37986; 21pp + Sequence Listing; English
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid
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                                                                                                                                                                              158 AAAAAALS 165
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2000US-0614150.
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genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 27429; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent
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                                                                                                                  Oryza sativa.
                                                                                                                                       Rice; Oryza sativa var. Kinmaze; acetolactic acid synthase; enzyme; herbicide resistance; pyrimidinylcarboxy-based herbicide; plant.
                                                                                                                                                                                                   30-AUG-2002
                                                                                                                                                                                                                           ABB81482;
                                                                                                                                                                                                                                                ABB81482 standard; Protein;
                                                                                             WO200244385-A1.
(TSUB ) KUMIAI CHEM IND CO LTD
                                                                      06-JUN-2002
                      29-NOV-2000; 2000JP-0362630
                                             16-NOV-2001; 2001WO-JP10014
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                                                                                                                                                                                                                                                                                                                                                      Conservative
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2000US-0614150
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                          468
                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                  644
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                                                                                                                                                                                                                                                                                                                                                                 Score 8;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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                                                                                                                                                                                                                                                                                                                                                                             Length 637;
                                                                                                                                                                                                                                                                                                                                                        Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents acetolactic acid synthase (I) isolate from Oryza sativa var. Klumaze (rice). (I) has resistance against pyrimidinylcarboxy (PC)-based herbicides as well as acetolactic acid synthase activity. (I) can be used for providing plants with high resistance against PC-based herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 82-86; 96pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene encoding acetolactic acid synthase, useful in providing ne of plants with high resistance against pyrimidinylcarboxy-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAAG-) NAT INST AGROBIOLOGICAL SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10024 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             herbicides
         This invention relates to novel nucleic acid and protein sequences of mutant acetohydroxyacid synthase (AHS) enzymes that can be used to create herbicide resistance green plants. The encoded AHAS exhibits resistance to at least one herbicide as compared to the wild-type, and has a serine-asparagine substitution at amino acid 627. The sequences of the invention are useful creating herbicide resistance plants, by
                                                                                                                                                                                                                                                                                                                                                                                                                Rice; AHS; acetohydroxyacid synthase; sulphonylurea herbicide; herbicide resistance; weed control; imidazolinone; EC.4.1.3.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice acetohydroxyacid synthase (AHS) wild type protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2002
                                                                                                                                                                                                                                                                                                            09-MAY-2001; 2001WO-US15072
                                                                                                                                                                                                                                                                                                                                                               WO200185970-A2
                                                                                                                                   herbicide resistant rice
                                                                                                                                                Novel gene encoding a functional acetohydroxyacid synthase gene which imparts resistance to at least one herbicide, used for producing
                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                      (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
                                                                                                                                                                                                                                                                                 10-MAY-2000; 2000US-203434P
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                                                                                                          Example 29; Page 117-119; 157pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Pred. No.
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these plants it is easier to control the growth of weeds in the

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Best Local
                   resistance to at least one harbicide as compared to the wild-type, and has a serine-asparagine substitution at amino acid 627. The sequences of the invention are useful creating herbicide resistance plants, by planting these plants it is easier to control the growth of weeds in the vicinity of a plant by applying a herbicide which normally inhibits AHAS. The sequences can be used for producing rice plants having resistance to at least one herbicide which normally inhibits AHAS in the wild-type plant, such herbicides may be particularly imidazolinone or sulphonylurea herbicides. The production of plant having resistance to AHAS inhibiting herbicide allows the development of new herbicides which harbicides may be particularly included the herbicides which herbicides of the production of grant having resistance to AHAS inhibiting herbicide allows the development of new herbicides which harget AHAS, reducing the risk of weeds becoming resistant. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vicinity of a plant by applying a herbicide which normally inhibits AHAS. The sequences can be used for producing rice plants having resistance to at least one herbicide which normally inhibits AHAS in the wild-type plant, such herbicides may be particularly inidazolinone or sulphonylurea herbicides. The production of plant having resistance to AHAS inhibiting herbicide allows the development of new herbicides which target AHAS, reducing the risk of weeds becoming resistant. The present sequence represents the wild type protein sequence of the rice AHS.
                                                                                                                                                                                                                                                                  This invention relates to novel nucleic acid and protein sequences
                                                                                                                                                                                                                                        create
                                                                                                                                                                                                                                                                                                            Disclosure; Page 121-123; 157pp;
                                                                                                                                                                                                                                                                                                                                                               Novel gene encoding a functional acetohydroxyacid synthase gene which imparts resistance to at least one herbicide, used for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAY-2001; 2001WO-US15072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice; AHS; acetohydroxyacid synthase; sulphonylurea herbicide; herbicide resistance; weed control; imidazolinone; EC.4.1.3.18;
                                                                                                                                                                                                                                                                                                                                                     herbicide resistant rice
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABK14658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Croughan TP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice herbicide resistant AHS protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU10025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme used to create the herbicide resistant plants of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-097559/13.
                                                                                                                                                                                                                              acetohydroxyacid synthase (AHS) enzymes that can be used to herbicide resistance green plants. The encoded AHAS exhibits
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8; Conserv
       represents
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the sequence of the mutant protein sequence
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                                            Sequence
                                                                                                     useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO18167-ABL30511), expressed DNA sequences (ABL01817-ABB72072).
                                                                               specification,
                                                                                                   sequences (ABL01840
(ABB57737-ABB72072)
                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                       The sequence data for this patent did not form
                                                                                                                                                                                                      Disclosure; SEQ ID NO 5082; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                     New isolated nucleic
                                                                                                                                                                                                                                                                             N-PSDB; ABL03533.
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11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rice AHS enzyme used to create the herbicide resistant plants of the
                                                                                                                                                                                                                                 interactions
                                                                                                                                                                                                                                          genes from Drosophila
                                                                                                                                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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             Local
                                                                 ftp.wipo.int/pub/published_pct_sequences
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Similarity 100.0%;
8; Conservative
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8; Conserv
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                                             662 AA;
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                                                                             but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                              PWD,
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          Score 8;
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Pred.
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL101676-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB57802 standard; Protein; 1164
                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 9621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001.
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                          Drosophila; developmental biology; cell signalling;
                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                        ABB60943 standard; Protein; 1412 AA
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                                insecticide;
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RESULT 26
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                      23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                          23-MAR-2001; 2001WO-US09231
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                                                                                                                                      Drosophila melanogaster
                                                                                                                                                               pharmaceutical.
                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 20838.
                                                                                                                                                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                           978 AAAAAALS 985
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2000US-0614150.
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Pred. No.
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(PEKE) PE CORP NY

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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                    New isolated nucleic acid
                                                                                           N-PSDB;
                                                                                                                               Venter JC,
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                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                       genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interactions
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8; Conserv
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                                                                                                                             Adams M,
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                                                    detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
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Pred. No.
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The invention relates

to an isolated nucleic acid detection reagent

Disclosure; SEQ ID NO 16689; 21pp + Sequence Listing;

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RESULT 28
AAW04637
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                                                                       responder cells that express TCR with a MHC ligand which stimulates the cells, and a test cpd.; (b) monitoring a signal produced by the cell when the TcR and MHC peptide ligand interact; and (c) comparing this signal with a control signal from a similar system lacking the test cpd. The specific inhibitors are potentially useful for blocking T-cells that cause autoimmune diseases (e.g. diabetes, rheumatoid arthritis, Grave's disease etc.), organ transplant rejection or other T cell mediated conditions. The interaction between a specific MHC peptide incard and a more credition in the condition of the periods in the condition of t
expressed on the surface of a basophil cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Specific inhibitors of interaction between T cell receptor and MHC peptide ligand - identified by incubating receptor expressing cells with ligand and test cpd., and measuring change in interaction to detect cpds. potentially useful for blocking disease related T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer; PCR; polymerase chain reaction; specific inhibitor;
T-cell receptor; TCR; MHC; ligand; autoimmune diseas; diabe
rheumatoid arthritis; Grave's disease; organ transplant rej
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                Novel specific inhibitors of the interaction between a T-cell receptor (TCR) and a MHC peptide ligand, are identified by: (a) incubating responder cells that express TCR with a MHC ligand which stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barouch DH,
                     ligand and a TCR was studied using purified MHC-single peptide complexes (e.g. AAW04633-37) and an antigen specific TCR-zeta chimeric receptor
                                                                                                                                                                                                                                                                                                                                                                                                           Example -; Page 3; 21pp;
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at ftp.wipo.int/pub/published_pct_sequences.
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-GB01165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCR; MHC; ligand; autoimmune diseas; diabetes; itls; Grave's disease; organ transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BK, Vessey SJR,
                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT 29
AAW61561
ID AAW61561
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XX IP-CCI
XX IP-
RESULT 30
AAR84046
ID AAR84
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AC AAR84
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Matches
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Best Local
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CTL clone
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     The biotinylated peptides AAW61559-W61561 were used in a peptide binding assay to test the peptide interactions of a Teol. Peptide derived from malaria can be used in an immunogenic composition. The T-cell epitope elicits an anti-malarial T-cell response in mammals of diverse genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 11; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09831382-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biotinylated peptide GYR(A)6L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW61561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW61561 standard; peptide;
                                     AAR84046 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                           backgrounds. The composition can be used as a vaccine to confer prophylactic or therapeutic immunity against malaria. They may also be used to inhibit the propagation of a malarial organism in a susceptible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunogenic compositions for malaria - comprise malaria derived peptide comprising universal T-cell epitope which elicits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-413810/35
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                                                                                                                                                                                                         Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAL 14
                                                                                                                                                                       AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAAL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to amplify TCR genes by PCR from cDNA prepared from specific for HLA A2.1 restricted HIV pol peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nardin E;
                                                                                                                                                                                                                                                                                       10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0033916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US01527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08; F1
                                                                                                                                                                                                                               4.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response
                                                                                                                                                                                                               0;
                                                                                                                                                                                                                               Score 7; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-malarial; prophylactic immunity.
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                               DB 19;
o. 11;
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es 0;
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                                                                                                                                                                                                                                                 Length 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                             Gaps
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   AAW02569
                                                                                                                                                                                                                                                                       RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A peptide of 7-30 amino acids capable of binding to a murine MHC class II mol. (i.e. AAR84018-47) covalently linked to 1-3 hapten mols. can be used for treating contact sensitivity, or desensitising a mammal to a contact allergen (e.g. urushiol of poison ivy/oak). The peptide-hapten cpds. disrupt the normal proliferation of hapten-specific T cells, or alter the T cell mediated delayed-type hypersensitivity response to the hapten,
                 Autoimmune disease; pACT59; pACT74; pACT36; pACT60; murine; T-cell; PKA; mouse; A-kinase anchoring protein 79; cAMP-dependent protein kinase; postsynaptic density; AKAP79; human forebrain; transcriptional activator; interleukin 2; T-cell activation; calcineurin; T-cell clonal expansion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gefter ML, Wilson KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; MHC class II; binding peptide; haptenated peptides; contact; sensitivity; desensitising; mammal; allergen; ivy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1996 (first entry)
                                                                                                                     AKAP79 A37-50 mutation.
                                                                                                                                                       13-JAN-1997
                                                                                                                                                                                             AAW02569;
                                                                                                                                                                                                                                   AAW02569 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 2; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haptenated peptide(s) capable of binding for treating contact dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-358583/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9526980-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       urushiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine
   calcium/calmodulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resulting in effective desensitisation to the hapten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating
                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                   7 IAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           poison; oak.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               class II binding peptide E5:10.
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                         (first entry)
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94US-0222206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "acylated"
   dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%;
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                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
   phosphatase; T-cell response;
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
lo. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hackett CJ;
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Class

II MHC molecules

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Gaps

0;

Length 13; Indels

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                                  Q
                                                                                                                                                                                     CC anchoring protein 79 (ARAP79). ARAP79 (see AAM05264 for wild type CC residues 37-50) is responsible for anchoring cAMP-dependent protein kinase CC (PKA) to specific intracellular sites. ARAP79 is predominantly present CC in postsynaptic densitles in the human forebrain. The pathways that CC in many cell functions, including the transcriptional activation of the context of the
                                                                                Matches
                                                                                               Query Match
Best Local (
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New modulators of anchoring protein function - used to develop prods. for use in the treatment of auto-immune-related conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW02565-W02569 represent mutants of residues 37-50 of the A-kinase anchoring protein 79 (AKAP79). AKAP79 (see AAW05264 for wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-268608/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; Page 34; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coghlan VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1995;
23-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09616172-A2
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(OREG-) STATE OF OREGON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune related disease; therapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                      æ
                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIV OREGON HEALTH
                     AAAAAAL 14
                                                                                                                                                             14
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallatin WM,
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94US-0344227.
95US-0404731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US16039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Lys50Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Lys45Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Lys42Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                      4.1%; Score 7; 1
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Lys41Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Arg40Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Arg39Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Howard ML,
                                                                          Mismatches
                                                                                           DB 17;
5. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lockerbie RO;
                                                                          0;
                                                                                                              Length 14
                                                                      0;
                                                                    Gaps
                                                                      0;
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RESULT 33 AAR84047

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G

Matches Query Match

Similarity

4.1%; Score 7; DB 21; 100.0%; Pred. No. 15; tive 0; Mismatches

Length 14;

0

Gaps

0;

Conservative

8 AAAAAAL 14

ΧIJ

AAR84047 standard; peptide; 16

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CC The present sequence is a mutant peptide derived from A-kinase anchor CC protein 79 (ARAP 79). It is expressed as a poly-histidine tag fusion CC protein 79 (ARAP 79). It is expressed as a poly-histidine tag fusion CC protein and can thus be purified to homogeneity by nickel affinity CC can calcineurin and so co-localises a kinase and a phosphatase that CC may regulate flux through a specific signalling pathway. Calcineurin is a CC2+/calmodulin-dependent protein phosphatase which is involved in many CC intracellular signalling pathways. It participates in regulation of IL-2 C expression following T cell stimulation in T cells. Calcineurin-binding CC peptides derived from AKAP 79 may be used to inhibit calcineurin activity CC in a cell. The peptides are useful for treating graft rejection following CC organ transplantation and for treating T cell-mediated disorders. CC Calcineurin deletion mutants which bind AKAP 79 are useful for defining CC an AKAP 79 binding site, for stimulating the immune response, stimulating cativated T cells for selected clonal expansion, or for enhancing T cell responses to experimental stimul for evaluation of early events in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1994;
15-MAR-1995;
17-JUL-1995;
Sequence
                                                              T cell biology and activation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Column 21; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel calcineurin deletion mutant having calcineurin polypeptide sequence and binding A-kinase anchor proteins, for treating graft rejection following organ transplantation and T cell-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; calcineurin-binding peptide; A-kinase anchor protein; AKAP; AKAP 79; immunostimulant; interleukin 2 expression modulation; graft rejection; transplantation; T cell-mediated disorder; mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-578541/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lockerbie RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6107104-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant peptide AKAP 79 A37-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB14909 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0344227
95US-0404731
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                                                                  immune
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                                                              response
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RESULT 34
ABB27942
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OS XXX AC XXX AC XXX
                                                                                                                                                                                                              Matches
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Best Local (
                                                                                                                                                                                                                                                                         A peptide of 7-30 amino acids capable of binding to a murine MHC class II mol. (i.e. AAR84018-47) covalently linked to 1-3 hapten mols. can be used for treating contact sensitivity, or desensitising a mammal to a contact allergen (e.g. urushiol of poison ivy/oak). The peptide-hapten cpds. disrupt the normal proliferation of hapten-specific T cells, or alter the T cell mediated delayed-type hypersensitivity response to the hapten, resulting in effective desensitisation to the hapten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urushiol; poison; oak.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine; MHC class II; binding peptide; haptenated peptides;
contact; sensitivity; desensitising; mammal; allergen; ivy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine MHC class II binding peptide E5:10:PDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR84047;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-358583/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gefter ML, Wilson KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-FEB-1995;
01-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09526980-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Haptenated peptide(s) capable of binding for treating contact dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMULOGIC PHARM CORP.
                                                                        01-FEB-2002
                                                                                             ABB27942;
                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 2; 85pp; English.
                               Human; microarray; single exon probe; gene expression; breast;
                                                   Human peptide #593 encoded by breast cell single exon nucleic acid
                                                                                                                 ABB27942 standard; Peptide; 21 AA.
                                                                                                                                                                                                                       Local
                                                                                                                                                                                                            l Similarity
7; Conserv
                                                                                                                                                                                  IAAAAAA 13
                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gelber C,
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                       (first entry)
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94US-0222206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US04121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "acylated"
                                                                                                                                                                                                                       4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greenstein
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                       Score 7; I
Pred. No.
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          JĽ,
                                                                                                                                                                                                                          DB 16;
). 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackett CJ;
                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                        Class II MHC molecules
                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                    Length 16
                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                 0;
   PN XXX
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RESULT 35
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Best Local (
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for eletermining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 10910; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                          04-FEB-2002 (first entry)
WO200157277-A2
                                                                                                       Peptide #5276 encoded by human foetal liver single exon probe.
                                                                                                                                                                              ABB37770;
                                                                                                                                                                                                                 ABB37770 standard; Peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                         130 NYLLGKG 136
                                                                                                                                                                                                                                                                                                          4 NYLLGKG
                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7;
                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT 36
AAM53912
          HORRES REPRESENTATION OF A CONTRACT CON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
     30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fetal liver. The present sequence is a peptide encoded by a succleic acid probe of the invention.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exor
                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                    W0200157275-A2
                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM53912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM53912 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 30405; 639pp + sequence listing; English.
                                                                                               26-MAY-2000;
                                                                                                                                                                      30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                        microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 NYLLGKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful for zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYLLGKG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AA;
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                    2000US-0180312.
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                                                                                                                                                                                                                                                                                                                                                                                     disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                   multiple
                                                                                                                                                                                                                                                                                                                                                                                                       expression analysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                              sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                          probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:
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AAM70864
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Best Local :
                                                                                                                                                                                        04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one continued to the process of the present sequence is a protein encoded by one continued to the process of the present sequence is a protein encoded.
                                                     Human genome-derived single exon nucleic acid probes useful
                                                                                                        Penn
                                                                                                                                                       04-OCT-2000;
                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
                                                                                                                             (MOLE-)
                                                                                                                                                                                                                                                     30-JAN-2001;
                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                  WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                  microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 31170.
                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM70864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM70864 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single
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les 7; Conser
                                                                                2001-488900/53.
                                                                                                        SG,
                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 NYLLGKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NYLLGKG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon nucleic acid
                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel
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                                                                                                                                                                2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                leukaemia; lymphoma;
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100.0%; Pred. No. 22;
                                                                                                     Chen W,
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                                                                                                      Rank DR;
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                                                                                                                                                                                                                                                                                                                                                myeloma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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The present invention provides a

Example 4;

SEQ ID NO:

31170; 658pp + Sequence Listing;

number

of single

exon

nucleic English.

acid

gene

expression

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marrow

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Best Local
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Query Match
Best Local Similarity
                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bone
                                                                                                                                                                                                                                             Claim 27; SEQ ID No 23534; 487pp; English.
                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #5142 encoded by probe for measuring cervical gene expression.
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                                           Sequence
                                                                                                                                                                                                                                                                                                                                                Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
                                                                                   specification,
                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 NYLLGKG 136
                                                                                     The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 NYLLGKG 10
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                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
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2000US-0207456.
2000US-050840B.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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100.08;
4.1%;
100.0%;
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 Score Pred.
                                                                                                                                                                                                                                                                                                                                                Rank DR;
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 . No.
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22;
 DB 22;
. 22;
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              Length 21;
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        ABG40662
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                      RESULT 40
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                                                                                                             Query Match
Best Local :
                                                                                                  Matches
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.
                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM26577 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #614 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-0CT-2001
                                                                                                                                             Sequence
                                                                                                                                                                human genetic disorders.
                                                                                                                                                                                                                                            Claim 27; SEQ ID No 26846; 654pp; English.
                                                                                                                                                                                                                                                                  analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                         Penn
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ABG40662 standard;
                                                                                                 Local Similarity
les 7; Conserv
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                                                                                                                                                                                                                                                                                                   2001-488897/53.
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                                                                            130 NYLLGKG 136
                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid
                                                      4 NYLLGKG
                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
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                                                                                                                                             21 AA;
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; 2000US-0236359.
; 2000GB-0024263.
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                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; placenta; antenatal diagnosis;
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                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                         Chen W,
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  21
                                                                                                             Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                          Rank DR;
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                                                                                                   Mismatches
                                                                                                              DB 22;
o. 22;
                                                                                                                                                                                                                                                                              probes
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                                                                                                                        Length 21;
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                                                                                                      Gaps
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19-AUG-2002

(first entry)

ABG40662;

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CC probes: Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a concleic acid expressed in the human lung; measuring gene expression in a CC sample derived from human lung; comparising the acriy with CC a collection of detectably labeled nucleic acids derived from human lung. Comprising (a) contacting the array with CC and collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with CC mRNA, and (b) measuring the label detectably bound to each probe of CC the array; identifying exons in a eukaryotic genome, comprising CC of the exharyote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, in the above mentioned microarray; assigning exons to a single exon probe, CC in the above mentioned microarray; assigning exons to a single gene, CC comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC itssues and/or cell types using hybridisation to a single exon CC expression of the exons in the tissues and/or cell types indicates that the expression of the exons in the tissues and/or cell types indicates that CC expression analysis, and for identifying exons in a gene, particularly cush muman lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease. CC Mieman-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary fice haemosiderosis, pulmonary histocytosis. lymbhandioleiomyomtosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-180312P.
26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234667P.
27-SEP-2000; 2000US-236559P.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
             pulmonary dysplasia,
                                         haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 30327; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        measure gene expression
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                      Sequence
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compug

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Result
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## ALIGNMENTS

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Infect. Immun. 59, 2515-2521, 1991
A;Title: Cloning, genetic analysis, and nucleotide sequence of a A;Reference number: A60337; MUID:91310296; PMID:1855972
A;Status: preliminary
                                                                                                                                                 submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Athors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Coliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A; Reference number: A59328
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A; Residues: 1-176 <LUD>
R; Engleberg, N.C.; Howe, D.C.; Rogers, J.E.; Arroyo, J.; Eisenstein, B.I.
Mol. Microbiol. 5, 2021-2029, 1991
Mol. Microbiol. 5, 2021-2029, 1991
Mol. Characterization of a Legionella pneumophila gene encoding a lipoprotein antige
A; Reference number: $16631; MUID:92114778; PMID:1766377
A; Recession: $16631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Legionella pneumophila
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carraro, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: E82625
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-186 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer membrane protein P6 precursor XF1896 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: E82625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000
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A; Residues: 1-176 <ENG>
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                                                                          A;Contents: annotation
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004009; GB:AE003849; NID:g9106980; PIDN:AAF84702.1; GSPDB:GN001
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conserved hypothetical protein SMa0520 [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence remission - . . .
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A; Title: The Drosophila toucan (toc) gene is required in A; Reference number: 217769; MUID:98090047; PMID:9362455 A; Accession: T13806
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Development 124, 4917-4926, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sugar-phosphate isomerase - Thermotoga maritima (strain MSB8)
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C; Species: Drosophila melanogaster
                                                                                                                                                                                           A; Experimental source: strain MSB8 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                        Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Thermotoga maritima
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                                                                                                                                                    A; Gene: TM1080 C; Superfamily: galactoside O-acetyltransferase
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A; Residues: 1-143 <ARN>
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                                                                                                                                                                                                                                                                                                                             A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
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20 NYLLGKGI 27
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                                                                                             4.7%;
100.0%;
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100.0%; Pred. No. 4.9;
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UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diamino-pimelate-D-alanyl-D-alanine C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #sext_change 03-Jun-2002 C;Accession: H81777
                                                                                                           RESULT
H81777
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C; Keywords:
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A; Residues: 1-381 <KIT>
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C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 02-Nov-2001
C;Accession: JC7650; pc7125
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A,Experimental source: strain 1021, megaplasmid pSyma
R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
habault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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Biosci. Biotechnol. Biochem. 65, 209-212, 2001
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A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Reference number: A95266; MUID:21396509; PMID:11481432
A; Accession: B95296
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A; Residues: 1-280 < KI
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R; Barnett, M.J.; Fi
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100.0%; Pred. No. 7.9
ative 0; Mismatches
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C;Keywords:
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A;Cross-references: EMBL:234883; NID:g1805667; PIDN:CAA84366.1; PID:g509467 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                               C; Superfamily: D-alanyl-D-alanine carboxypeptidase
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A; Cross-references: GB:
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: 140455; D69673; S49132
                                                                                                                                                                                                                                                                      A; Experimental source: strain
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                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown; translation not shown
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A;Residues: 1-452 <PAR>
A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85286.1; PID:g738
A;Experimental source: serogroup A, strain 22491
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A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-491 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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       Conservative
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                                                                                                                                                                                                                                                                  GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13718.1; PID:g26342
ce: strain 168
                                       4.7%; Score 8; 1
100.0%; Pred. No.
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Pred. No.
   Mismatches
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                                                                       DB 2;
                                                                       Length 491;
0;
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Indels
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Cell 61, 85-99, 1990
A;Title: The Drosophila 74EF early puff contains E74, a A;Reference number: A90912; MUID:90199900; PMID:2107982 A;Accession: A34692 A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: ditE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 181, 2675-2682, 1999
A;Title: A novel aromatic-ring-hydroxylating dioxygenase from
A;Reference number: Z25281; MUID:99235742; PMID:10217753
A;Accession: T50939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DitE protein [imported] - Pseudomonas abietaniphila C;Species: Pseudomonas abietaniphila C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: T50939
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C; Superfamily: dipeptide transport protein
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A;Reference number: A82950;
A;Accession: G82981
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Nature 406, 959-964, 2000
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                  N;Alternate names: ets-related protein E74A
C;Specias: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Sep-1998
C;Accession: A34692
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A; Residues: 1-547 < MAR>
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A; Residues: 1-526 <STO>
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                                                                                               R;Burtis, K.C.; Thumm
Cell 61, 85-99, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF119621; PIDN:AAD21067.1
A;Experimental source: strain BKME-9; ATCC700689
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                                                                                                                                                                                                                                                                               A34692
                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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nes 8; Conserv
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8; Conserv
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                                                                                                                                Thummel, C.S.; Jones, C.W.; Karim, F.D.; Hogness, D.S.
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50; MUID:20437337; PMID:10984043
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A;Residues: 1-829 <BUR>
A;Cross references: GB:M37082; NID:g157307; PID:g157308
C;Genetics:
A;Gene: E74
A;Cross references: FlyBase:FBgn0000567
C;Superfamily: ets DNA-binding domain homology
C;Keywords: alternative splicing; DNA binding; nucleus;
F;735-815/Domain: ets DNA-binding domain homology <ETS>
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                               Biochim. Biophys. Acta 495, 388-392, 1977
A;Title: Structure of a peptide antifreeze and mechanism A;Reference number: A03192; MUID:78060969; PMID:588591
A;Accession: A03192
                                                                                                                                                                                                                                                                                                                          antifreeze protein 3 - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
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A; Residues: 1-2715 <TRE>
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A; Accession: T13049
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R; Treisman, J.E.;
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                                                                                                                                             C; Keywords: antifreeze
                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1-37 <DEV>
                                                                                                                                                                                                                                                                                        R; DeVries, A.L.; Lin, Y.
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                                                                                                                                                              ;Superfamily: antifreeze
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                                                                   Local Similarity es 7; Conserv
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C:Genetics: 19/2
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Reywords: antifreeze; plasma; tandem repeat
F:1-21/Comain: signal sequence #status predicted <SIG>F:22-44/Domain: propeptide #status predicted <PRO>F:45-82/Product: antifreeze protein A #status predicted <WAT>
                           antifreeze protein A - winter flounder (*):Species: Pseudopleuronectes americanus (winter flounder) C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 24-Oct-2000 C:Accession: S02326; JH0627
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                                                                                                                           RESULT 16
S02326
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A;Residues: 1-40 <CHA>
C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end
F;l/Modified site: blocked amino end (Met) #status experimental
       R; Scott, G.K.; Davies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: JS0704
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C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
C;Accession: JS0704; A03194
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C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-82 <DA1>
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A; Accession: S07046
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R; Chakrabartty, A.; Hew, C.L.; Can. J. Zool. 66, 403-408, 1988
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P.L.; Kao, M.H.; Fletcher, G.L.
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100.0%; Pred. No.
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A; Molecule type: DNA
A; Residues: 1-82 <DAV>
                                                                                                                 R;Davies, P.L.; Hough, C.; Scott, G.K.; Ng, N.; White, B.N.; Hew, C.L. J. Biol. Chem. 259, 9241-9247, 1984
A;Reference number: A05161; MUID:84264559; PMID:6086629
                                                                                                                                                                                                   antifreeze protein B precursor - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 24-Oct-2000
A; Introns: 19/2
                                      A; Cross-references:
                                                                                                      A; Accession: A05161
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Gene 112, 163-170, 1992
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C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
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C; Superfamily: antifreeze protein
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A; Residues: 1-82 <DAV>
A; Cross-references: GB:M62417;
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C;Keywords: antifreeze
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A.Title: Differential amplification of antifreeze protein genes in the Pleuronectinae
A.Reference number: S02326; MUID:88259236; PMID:3133486
A.Recession: S02326
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A; Residues: 1-82 < DAV>
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A;Accession: JH0627
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Gene 112, 163-170,
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A; Residues: 1-82 <SCO>
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                                                                                                                                                                                          Accession: A05161
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                               GB:L00138; GB:J00929; NID:g343126; PIDN:AAB59964.1; PID:g457351
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A;Title: Conservation of antifreeze protein-encoding genes A;Reference number: JH0627; MUID:92209995; PMID:1555765 A;Accession: JS0705 A;Molecule type: DNA A;Residues: 1-82 <DAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antifreeze protein (clones 1A-1a and 3-3a) - winter flounder
C; Species: Pseudopleuronectes americanus (winter flounder)
C; Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
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C;Keywords: antifreeze
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze
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                                                                                                                                                                                                                                                                                                                                                                                                                R;Pickett, M.; Scott, G.; Davies, P.; Wang, N.; Joshi, S.; Hew, C. Eur. J. Biochem. 143, 35-38, 1984
A;Title: Sequence of an antifreeze protein precursor.
A;Reference number: IS1125; MUID:84285392; PMID:6547905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Oct-2000
C;Accession: I51125
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oppF homolog, kgmB 5'-region -
C; Species: Streptomyces tenebra
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C;Keywords: antifreeze
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                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-82 <PIC>
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                                    A55846
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                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 AAAAAAL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ
                                                                                                            50 AAAAAAL 56
                                                                                                                                                                               l Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAL 14
                                                                                                                                                 AAAAAAL 14
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                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
 tenebrarius
                                                                                                                                                                                                    4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1%;
                 Streptomyces tenebrarius (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; 1; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                     0;
                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                      DB 2;
o. 25;
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5. 25;
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                                                                                                                                                                                                                       Length 82
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                                                                                                                                                                                     0;
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hypothetical protein Rv2719c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70533

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: B70533

A;Cross-references: GB:296072; GB:AL123456; NID:g3261793; PIDN:CAB09460.1; PID:g21820

A; Experimental source: strain

A; Molecule type: DNA A; Residues: 1-165 <COL>

A; Status: preliminary; nucleic acid sequence not shown;

translation not shown

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar 2001 #sequence_revision 02-Mar 2001 #text_change 31-Dec-2001
C;Accession: F86299
R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-May-1995 C;Accession: A55846 R;Holmes, D.J.; Cundliffe, E. Mol. Gen. Genet. 229, 229-237, 1991 Mol. Gen. Analysis of a ribosomal RNA methylase gene from Streptomyces tenebrarius whi A;Reference number: S17717; MUID:92017656; PMID:1921972 A;Accession: A55846
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A; Residues: 1-87 <HOL>
  В
                                                                                                                                                                                                                   A; Map position: 1
                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005172; NID:g4966364; PIDN:AAD34695.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F309.23 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-150 <STO>
                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                         Query Match
                                                                                                                                       Local
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17 AAAAAAL 23
                                                                                                     l Similarity
7; Conserva
                                                      8 AAAAAAL 14
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                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                                     4.1%;
                                                                                                             0;
                                                                                                                                     Score 7; DB 2; Pred. No. 43;
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                                                                                                                Indels
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                                                                                                                   Gaps
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C; Species:
                                         omp16 protein - Brucella abortus
                                                                                           RESULT 26
                                                                                                                                                               Дb
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                                                                                                                                                                                                                                                                                                                                     A;Gene: oprL; PA0973
C;Superfamily: outer membrane protein A
                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04362.1; GSPDB:GN00-A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-168 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer membrane protein OprL precursor PA0973 [imported] - Pseudomonas aeruginosa (strair C;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: G83525
                                                                        140346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A82950; A; Accession: G83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A; Reference number: A82950; MUID:20437337; PMID:10984043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-167 <LIM>
A; Cross_references: EMBL: Z50191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: outer membrane protein A
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A; Accession: S58217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Pseudomonas aeruginosa
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 26-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: Molecular cloning, nucleotide sequence, and characterization of OprL, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S58217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outer membrane protein - Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                          102 GHTDERG 108
                                                                                                                                                                                                        106 GHTDERG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 GHTDERG 112
                   Brucella abortus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 VAPNAPT 136
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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100.0%; Pre
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100.0%; Pred. No.
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Pred. No.
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Pred. No. 46;
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                                                                                                                                                                                                                                                                    DB 2;
5. 47;
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                                                                                                                                                                                                                                                                                          Length 168;
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                                                                                  DNA Res. 8, 205-213, 2001

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2405
A;Cross-references: GB:BA000019; PIDN:BAB76496.1; PID:g17133934; GSPDB:GN00179 A;Experimental source: strain PCC 7120
                                                                                                                                                                                    C;Accession: AE2405
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                      A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                  A; Molecule type: DNA A; Residues: 1-170 < KUR>
                                                                                                                                                                                                                                                                                                                                     hypothetical protein all4797 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                              AE2405
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Species: Nostoc sp.

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                                                                                                                                                                                      A; Map position: I
C; Superfamily: outer membrane protein A
                                             QУ
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                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE008917; PIDN:AAL51521.1; PID:g17982237; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA A; Residues: 1-168 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                          ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, Š.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
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A;Title: Molecular cloning, nucleotide sequence, and occurrence of a 16.5-kilodalton A;Reference number: 140346; MUID:94341863; PMID:8063379
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C;Accession: I40346
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153 WSQNRRA 159
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EUR. J. Biochem. 163, 73–77, 1987
A,Title: Nucleotide sequence of the gene for the peptidoglycan-associated lipoprotein of
A;Reference number: A27534; MUID:87133578; PMID:3545827
A;Accession: A27534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: pal; excC
A;Map position: 17 min
A;Map position: 17 min
C;Superfamily: outer membrane protein A
C;Keywords: lipid binding; lipoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-173/Product: peptidoglycan-associated lipoprotein #status predicted <MAT>
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A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Recession: D64810
A; Status: nucleic acid sequence not shown; translation not shown
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C;Date: 30-Sep-1988 *sequence_revision 30-Sep-1988 *text_change 01-Mar-2002
C;Accession: A27534; S20547; D64810
R;Chen, R; Henning, U.
Eur. J. Biochem. 163, 73-77, 1987
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C; Species: Escherichia coli
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A; Gene: all4797
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A;Title: The excC gene of Escherichia coli K-12 required for cell envelope integrity end A;Reference number: S20546; MUID:92244043; PMID:1574003
A;Accession: S20547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X65796; NID:g41358; PIDN:CAA46673.1; PID:g41360 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V
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A; Residues: 1-173 <BLAT>
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A; Residues: 1-173 <LAZ>
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                       iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
                                                                       C;Accession: A85577
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner,
                                                                                                                       C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 01-Mar-2002
                                                                                                                                                                          peptidoglycan-associated lipoprotein [imported] - Escherichia coli (strain 0157:H7,
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A;Accession: A85577
A;Status: preliminary
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                                                                                                                                                                                                                                                                              Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: AB0502; PMID:11677608
A; Accession: A10592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptidoglycan-associated lipoprotein precursor [imported] - Salmonella enter C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 01-Mar-2002 C; Accession: AI0592
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Experimental source: strain 0157:H7, substrain EDL933
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A; Residues: 1-173 <HAY>
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A;Gene: STY0/95
C;Superfamily: outer membrane protein A
                                                                                                               A;Cross-references: GB:AL513382; PIDN:CAD05211.1;
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A; Residues: 1-174 < PAR>
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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
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                                                                                 C; Genetics:
                                                                                                                                                                                                                                            A; Status: preliminary
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nes 7; Conserv
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N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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Pred. No.
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                                                                                                                                     PID:g16501981;
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omp16 protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AJ011044; PIDN:CAB55622.1 A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-176 <HAT>
A; Cross-references: EMBI
                                                           AE3013
                                                                                                                                                                                                                                                                                                                                                                           A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cysteine synthase (EC 4.2.99.8), mitochondrial [imported] - Arabidopsis thaliana (fragme C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000 C;Accession: T52661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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Plant Physiol. 123, 1163-1171, 2000
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A; Residues: 1-174 <KAW>
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A;Reference number: A72450; MUID:99310339; PMID:10382966
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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
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C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: F72550
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100.0%; Pred. No. 48
tive 0; Mismatches
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100.0%; Pred. No. 48;
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M.; Shen, M.; Vamathevan, J.J.; Lam, P.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: D75351
                                                                                                                                                                                                        C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                      R; White, O.; Eisen,
                                                                                                                                                                                                                                                                 probable acetyltransferase - Deinococcus radiodurans (strain R1)
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    omp16 protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 01-Mar-2002
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A; Residues: 1-177 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status:
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A; Residues: 1-177 < KUR>
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Local Similarity 100.0%; F
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                                                                                                                            J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, athevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
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%; Pred. No. 49;
0; Mismatches
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Fereira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu, C.H.; Martino, C.L.; Marques, M.V.; Martins, H.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.A.; Aluthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; F.G.; Nunes, V.; Rosa, A.J.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak R.; Aluthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, R.G.; Santelli, R.V.; Sawasak A; Aluthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, R.G.; Palmieri, D.A.; da Silva, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
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C;Superfamily: Escherichia coli ribosomal-protein-alanine N-acetyltransferase rimJ
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A; Residues: 1-179 <WHI>
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A;Status: preliminary
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A;Residues: 1-185 <SIM>
A;Cross-references: GB:AE003927; GB:AE003849; NID:g9105783; PIDN:AAF83693.1; GSPDB:GN001
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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trace, Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71495
                                                                                                                                                                                 probable peptidoglycan-associated lipoprotein - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2000 C;Accession: E71495
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                                                                                                                R;Stephens, R.S.; Kalman, Science 282, 754-759, 1998
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                                                                                                                                                  Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
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100.0%; Pred. No.
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100.0%; Pred. No.
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-188 <ARN>
A;Residues: 1-188 <ARN>
A;Cross-references: GB:AE001330; GB:AE001273; NID:g3329034; PIDN:AAC68202.1; PID:g332
A;Cross-references: GB:AE001330; GB:AE001273; NID:g3329034; PIDN:AAC68202.1; PID:g332
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A;Gene: pal
C;Superfamily: outer membrane protein A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001659; GB:AE001363; NID:g4377081; PIDN:AAD18919.1; PID:g437 A;Experimental source: strain CWL029 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke R;Read, T.D.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000 DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nicleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
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                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE002265; GB:AE002161; NID:g7189999; PIDN:AAF38862.1; PID:g719
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A;Accession: C81504
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                                                                                                                                                                                                                                             C; Superfamily: outer membrane protein A
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                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-192 < REA>
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A; Residues: 1-192 <ARN>
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                                                                                                                        Local Similarity 100.0%; les 7; Conservative
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123 GHTDERG 129
                                                             106 GHTDERG 112
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100.0%; Pred. No.
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AAB46316
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H. pylori outer me Expressed antigen H. pylori outer me Expressed antigen H. pylori uter me Expressed antigen H. pylori uter me protein encoded by H. pylori omp22 ou H. pylori recombin Chlamydia pneumoni Chlamydia pneumoni Expressed antigen Chlamydia trachoma Momp P5. Heamophi Ph. aeruginosa orpf Nontypable H. infl Protein associated Actinobacillus ple Protein associated Actinobacillus ple Actinobacillus ple Protein associated Actinobacillus ple Actinobacillus paraga Haemophilus para

Escherichia

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BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists of antagonists and antagonists and antagonists of the treatment and prevention of diseases including bacterial infection, otitis media in infants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. catarrhalis BASB019 protein sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY55089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY55089 standard; Protein; 172 AA
                                                                                                 This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for
                                                                                                                                                                                                              WPI; 2000-062148/05.
N-PSDB; AAZ40351.
                                                                                                                                                                                                                                                                                          06-MAY-1998;
                                                                                                                                                                                                                                                                                                                03-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis.
                                                                                                                                                                              Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                               Ruelle J
                                                                                                                                                         Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                             screening of genetic mutations, serotype, organism or strain identification of mutation in BASB013 sequences, and as
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AAB09475
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Novel
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Soluble Porphyromo
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY55090 standard; Protein; 172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistant bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY55090;
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                                                                                                                                                                                                                                                                                                                                                                           Moraxella catarrhalis.
                                                                Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS:
                                                                                                                                                                                                                                                                                                                                           W09957277-A2
                                  Claim 3; Fig 3; 101pp; English.
                                                                                                                   N-PSDB; AAZ40352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Pred. No. 8.7e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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This sequence is a Moraxella catarrhalis BASB019 protein of the

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RESULT 3
AAX75091
ID AAX5
XX AAX5
AC AAX5
XX AX
DT 01-M
XX BASB
KW BASB
KW Gene
KW Inva
KW Inva
KW Uppe
OS MOTA
XX WO99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC invention. The sequences can be used for diagnosis of disease, staging of CC disease, or determining response of an infectious organism to drugs. The CC disease, or determining response of an infectious organism to drugs. The CC polynucleotides may be used as a source for hybridisation probes, and for CC components of genetic mutations, serotype, organism or strain CC components of arrays which are useful for diagnostic and prognostic CC purposes. The polypeptides can be used to produce antibodies, and as CC also be used in vaccine formulations, and to identify agonists and CC also be used in vaccine formulations, and to identify agonists and CC (which are bacteristatic) are used for the treatment and prevention of CC diseases including bacterial infection, otitis media in infants and CC invasive diseases, chronic otitis media with hearing loss, fluid CC accumulation in the elderly, sinusitis, noscomial infections and CC learning, infection of the upper respiratory tract and middle ear CC infection. They are also used in the prevention of adhesion of bacteria CC control of infections on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the implantation of pathogenesis in infections initiated other than by the implantation of pathogenesis in infections has risen dramatically, can be used screen for new antibacterial compounds that may target these CC resistant to standard antibiotics. The BASBO19 products of the invention CC can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                             03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. catarrhalis BASB019 protein sequence #3.
                                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY55091 standard; Protein; 172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ALASTLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MMLHIQIAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMLHIQIAAAAAALSVLTFWTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                  98GB-0009683.
                                                                                                                                     99WO-EP03038
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99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 855; DB 21; Length 172; Pred. No. 4e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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В Ş Dр δõ B

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This sequence is a Moraxella catarrhalis BASBO19 protein of the CC invention. The sequences can be used for diagnosis of disease, staging of components or determining response of an infectious organism to drugs. The CC polynucleotides may be used as a source for hybridisation probes, and for cidentification, identification of mutation in BASBO13 sequences, and as components of arrays which are useful for diagnostic and prognostic CC purposes. The polypeptides can be used to produce antibodies, and as a cc also be used in vaccine formulations, and to identify agonists and CC also be used in vaccine formulations, and to identify agonists and cc diseases including bacterial infection, oticis media in infants and CC diseases including bacterial infection, oticis media in infants and cc invasive diseases, chronic otits media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech CC infection. They are also used in the prevention of adhesion of bacteria cc infections on in-dwelling devices, or to extracellular cc proteins on wounds, and to thus prevent tissue damage and/or block the companiency of Moraxella catarrhalis infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections initiated other than by crast that to standard antibiotics. The BASBO19 products of the invention of these used screen for new antibacterial compounds that may threet these
Sequence
                                                    can be used screen for new antibacterial compounds that may target
                                               resistant bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel BASB019 polynucleotides and polypeptides from Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruelle J;
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  172 AA;
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В
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                                                                                                                                                           В
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                                                                                                                                                                                                                                  Matches
                   121 GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
             121
                                                                     61 TLASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL
                                                                                                     61 ALASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL 120
                                                                                                                                                                                                                                169;
                                                                                                                                          1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETIK 60
                                                                                                                                                             1 MMLHIQIAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                     0;
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Query Match Best Local :

Similarity

98.3%;

98.7%; Score 850; DB 21; 98.3%; Pred. No. 1.4e-84;

DB 21;

Length 172;

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KW KW XE XE XXX
                                                                                                                                                                                                                                                                                   AAY55092
                                                                                                                                                                                                                                                                                                        RESULT 4
BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                              M. catarrhalis BASB019 protein sequence #4.
                                                                                                                                                                                01-MAR-2000
                                                                                                                                                                                                                                                     AAY55092 standard; Protein; 172 AA.
                                                                                                                                                                       (first entry)
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS

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XX PD XX XX PD XX XX
RESULT 5
AAR07145
ID AAR0
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                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists and arrays are used for the treatment and prevention of diseases including bacterial infection, otitis media in infants and children, pneumonia in the elderly, sinusitis, nosocomial infections and invasive diseases, chronic otitis media with hearing loss, fluid invasive diseases, chronic otitis media with hearing loss, fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accumulation in the middle ear, auditive nerve damage, delayed speech learning, infection of the upper respiratory tract and middle ear infection. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogeness in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M. catarrhalis strains that are resistant to standard antibiotics. The BASBO19 products of the invention can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09957277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynicleotides may be used as a source for hybridisation probes, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ40354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-062148/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
  AAR07145 standard; protein; 153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resistant bacteria
                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                169; Conservative
                                                                                                                                                                                           61 ALASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL 120
                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                   \vdash
                                                                                                                                                                                                                                                                                                                        1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                              GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                      ALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL 120
                                                                                                                                                                                                                                                                                 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYAGVIYTGVAPLVDNDETVK
                                                                                                        GERRAVAVRNYLLSKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98GB-0009683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-EP03038.
                                                                                                                                                                                                                                                                                                                                                                                           98.0%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                           Score 844; DB 21; Length 172; pred. No. 6.3e-84;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                              0;
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DE XXX PPN XXX
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AAP82947
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PD XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6kD outer membrane protein (OMP) of H.influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR07145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purification of outer membrane protein of haemophilus influenzae
   by separation from an insoluble fraction using
detergent-contg., then detergent-free buffers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy TF, Apicella MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP389925-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-298924/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNE-) STATE UNIV NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H.influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method claimed produces large quantities of the purified OMP, useful in raising antibodies for detection, and as a vaccine against
                                                                                                                                                                                                          AAP82947 standard; protein; 153 AA
                                                                                                                      16600 dalton outer membrane protein of non-typable H influenzae.
                                                                                                                                                                                AAP82947;
                           EP281673-A.
                                                      Haemophilus influenzae
                                                                               pneumonia; meningitis; ss.
                                                                                            Haemophilus influenzae; 16600 dalton outer membrane protein (OMP);
                                                                                                                                                     10-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                              105 RADAVKGYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                        124 RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                    51 -----VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQR
                                                                                                                                                                                                                                                                                                                                                              64 SKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGER 123
                                                                                                                                                                                                                                                                                                                                                                                                                      25 NKSTSQVMVAPNAPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                         2 NKFVKSLLVAGSVPALAACSSSNNDAAGNGAAQSFGGYS-----VADLQQRYNT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ07145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0330229
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                                                                                                                                                                                                                                                                                                                                                                                                                                               30.9%; Score 266; DB 11; Length 153; 36.7%; Pred. No. 6.5e-21; Live 24; Mismatches 45; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                         -------GYTGVIYTGVAPLVDNDETVKALA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Gaps
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14-SEP-1988

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RESULT 7
AAP80593
ID AAP8
XX AAP8
AC AAP8
AC AAP8
XX Haen
CX Haen
KW Pnet
CXX Haen
XX 
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                                                                                                                                                                                                                                                                                        08-OCT-1987;
08-NOV-1986;
        Plasmids, E.coli, hybridomas and antibodies from H.influenzae protein for use as vaccine and detection of Haemophilus influenzae
                                                                                                   N-PSDB; AAN81194.
                                                                                                                                                                                Murphy TF,
                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16600 dalton outer membrane protein of non-typable H influenzae.
                                                                                                                                                                                                                                    (UYNY-) RES UNIV NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumonia; meningitis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae; 16600 dalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP80593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP80593 standard; protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An epitope of this protein is recognised by the 7F3 antibody in a number of isolates. Monoclonal antibodies to the 16600 D OMP are produced by hybridomas and used to detect H.influenzae. A suspect sample is contacted with the MAb in the presence of an indicator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as radiolabelled probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; ; ; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmids, E.coli, hybridomas and antibodies from H.influenzae protein for use as vaccine and detection of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1988-258472/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1987;
08-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy TF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNY-) RES UNIV NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                           1988-258472/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN81194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 AA;
                                                                                                                                                                                Apicella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apicella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                   87US-0092948
86US-0932872
                                                                                                                                                                                                                                                                                                                                                                87EP-0116699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87US-0092948
86US-0932872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 264; DB 9;
Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer membrane protein (OMP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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AXX CCCCCCCCCCXXX PTT XXX PTX X PTX 
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AAR05797
ID AARC
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                                       The PBOMP proteins were isolated from a PBOMP-enriched insoluble cell wall fraction from physically disrupted cells of H. influenzae and then solubilising the PBOMP from the cell wall fraction by heating in the presence of a detergent or digesting the cell wall fraction with lysozyme, opt. in the presence of a detergent. The genes encoding the PBOMP proteins were isolated by screening a DNA library with an oligonucleotide probe based on the amino acid sequence of the PBOMP protein, or using antibodies to PBOMP.
                                                                                                                                                                                                                                                                                                              Disclosure; Fig 11; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane protein epitopes of Haemophilus influenzae- used in the prodn. of antibodies, in vaccines and for prodn. of reagents for
                                                                                                                                                                                                                                                                                                                                                                           diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ03869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anilionis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-1988;
21-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PRAX-) PRAXIS BIOLOGICS IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09002557-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Praxis Biologics Outer Membrane Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane proteins; PBOMP-1; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An epitope of this protein is recognised by the 7F3 antibody in a number of isolates. Monoclonal antibodies to the 16600 D OMP are produced by hybridomas and used to detect H.influenzae. A suspect sample is contacted with the MAb in the presence of an indicator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PBOMP-1 gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR05797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as radiolabelled probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1990-115815/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 VYFDFDSDEIKPQAAAILDEQAQFLITNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seid RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88US-0239572
89US-0396572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 264; DB 9;
Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zlotnick GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green
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                                                                                                                                                                                                                                                                                                                                                                                                reagents for
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Query Match Best Local Similarity

30.7%; 49.5%;

Score 264; DB 11; Pred. No. 1.1e-20;

Length 153;

Sequence

153

AA;

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AARSSULX
AA
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                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1986;
08-OCT-1987;
29-MAR-1989;
12-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification; pneumonia; bacteraemia; meningitis;
postpartum sepsis; acute febrile tracheobronchitis; neonatal sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane protein; vaccine; antibody; treatment; identification; pneumonia; bacteraemia; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                  The P6 outer membrane protein (OMP) is conserved among strains of Haemophilus influenzas and so antibodies to the OMP can be used to identify H. influenzas in clinical samples. The OMP can also be used in the development of vaccines against H. influenzas which causes pneumonia, bacteraemia, meningitis, postpartum sepsis and acute febrile tracheobronchitis in adults and neonatal sepsis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR51161 standard; Protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purifying outer membrane protein of Haemophilus influenzae extn. with detergent buffer, treatment with RNase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-109467/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1994
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Figure 11b; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    solubilising by heat-treating in detergent-free buffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR51161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apicella MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNY ) UNIV NEW YORK STATE RES
                                                                                                                                                                                                                                                                                                                                                                                                             acute otitis media in infants and children
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GYLAGKGYDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane protein P6 of Haemophilus influenzae
111 GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY
                                                         130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            otitis media; Haemophilus influenzae; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
                                                                                                                   VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
                                                                                                                                                                         VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                      153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86US-0932872.
87US-0092948.
89US-0330229.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86US-0932872
                                                                                                                                                                                                                                                           30.7%;
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                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                              Score 264; DB 15;
Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                             Length 153;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection;
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AAW20394 ID AAW

AAW20394 standard;

Protein;

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AAW20394;

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RESULT 10
AAP80665
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                                                                                                      Query Match
Best Local (
                                                                                            Matches
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02-MAR-1987;
31-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP80665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP80665 standard;
                                                                                                                                                                         A pure antigenic peptide or protein related to an epitope of Haemophilu influenzae is claimed. Also claimed is a recombinant vector comprising DNA sequence coding for an antigenic determinant of an Haemophilus influenzae outer membrane protein, the transformed cell, a subunit vaccine in a pharmaceutical carrier, a method of immunising humans and
                                                                                                                                                                                                                                                                      Pure peptide related to epitope of Haemophilus influenzae used as immunogens in vaccines and for producing antibodis passive immunisation and assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO8804932-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; diagnosis; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoded
                                                                                                                                          Sequence
                                                                                                                                                                 an assay for Haemophilus influenzae.
                                                                                                                                                                                                                                                 Disclosure; Fig 11; 129pp; English.
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAN80226
                                                                                                                                                                                                                                                                                                                                                         Deich RA,
                                                                                                                                                                                                                                                                                                                                                                              (PRAX-) PRAXIS BIOLOGICS IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                 1988-205305/29.
                      130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                51
                                                           70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                             50;
                                                                                                          Similarity
GYLAGKGVDAGKLGTVSYGEEKPAVLGHDESAYSKNRRAVLAY 153
                                             VYLGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PBOMP-1)
                                                                                                                                            153 AA;
                                                                                                                                                                                                                                                                                                                                                         Zlotnick G,
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    87US-0132073.
87US-0020849.
86US-0948364.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene.
                                                                                                       30.1%;
                                                                                                                                                                                                                                                                                                                                                          Green
                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           influenzae Praxis Biolgics Outer Membrane
                                                                                                          Score 259; DB 9;
Pred. No. 3.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunisation
                                                                                                                   Length 153;
                                                                                                                                                                                                                                                                                     antibodies
                                                                                                                                                                                                                                                                                         for
                                                                                              0;
                                                                                                                                                                                                                 Haemophilus
comprising a
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29-JUL-1997 (first entry)

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                                                                                                                                                                                                                                                                                  δÃ
                                                AAW24651
                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a H. pylori outer membrane protein.

The protein may be used in a vaccine to prevent or treat H. pylori
C infection or to identify H. pylori polypeptide binding compounds,
U useful as potential H. pylori life cycle activators or inhibitors.
C werlapping contigs generated by mechanically shearing the bacterial
C DNA. The sequences were analysed for ORF of at least 180 nucleotides,
and the predicted coding regions defined by computer evaluation. To
C dentify likely H. pylori antigens for vaccine development, the amino
acid sequences predicted from various ORF were analysed for significant
homology to other known or exported membrane proteins. Having identified
and determined the sequences of interest, particular regions can be
isolated from H. pylori by PCR amplification for recombinant polypeptide
production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
AAW24651;
                     AAW24651 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 56; Page 577; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT67789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09640893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H. pylori outer membrane protein 31262.aa.
                                                                                                                                   117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                    122 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVQKTRECYRENRRVDV 175
                                                                                                                                                                     65 PAIE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                                                                     57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                                                                                                       15 SVLIFM-----TGCANK------STSQVMVAP--NAPTGYTGVIYTGVAPLVDND 56
                                                                                                                                                                                                                                       5 SVFSFLVAFLLVVGCSHKMDNKTVAGDVSTKAVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                       179 AA;
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0630405
95US-0487032
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                                                                                                                                                                                                                                                                                                                                 25.0%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                               Score 215.5; DB Pred. No. 2.6e-15
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                            DB 18; Length 179;
                                                                                                                                                                                                                                                                                                               66;
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                                                                                                                                                                                                                                                                                                                                                                              also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of shotgum subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are used to evaluate compounds, especially activators or inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents an H. pylori outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 171; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori nucleic acid sequences and related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT77469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-298052/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; antisense; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASTR ) ASTRA AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. pylori outer membrane protein 31262.aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-1997 (first entry)
                                                                                                                                                                                                                                                  Local
122 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVQKTRECYRENRRVDV 175
                                 117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                     the related specification, W09640893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diagnostics and therapeutics
                                                                      65 PAIE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                         57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                               15 SVLTFM-----TGCANK------STSQVMVAP--NAPTGYTGVIYTGVAPLVDND 56
                                                                                                                                                                                                                                                                                                                                               The ORF/protein reference number for this sequence was obtained
                                                                                                                                            5 SVFSFLVAFLLVVGCSHKMDNKTVAGDVSTKAVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                      179 AA;
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0561469
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                                                                                                                                                                                                                                        25.0%; Score 215.5; DB 18; Length 179; 32.8%; Pred. No. 2.6e-15;
                                                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                          66;
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RESULT 14
AAB46316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed antigen for clone Y175A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW89982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW89982 standard; Protein; 179 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 321; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1998;
05-APR-2001
                                   AAB46316;
                                                                    AAB46316 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                           117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                              65 PAVE---SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                                                                                                                               57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                                                                                                                                                                  15 SYLTFM------TGCANKSTSQVMVAP-NAPTGYTGVIYT-------GVAPLVDND 56
                                                                                                                                                                                                                                                                                                  SVFSFLVAFLLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                                                         NQALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0061958.
97US-0045107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US08487
                                                                                                                                                                                                                                                                                                                                                                       25.0%; Score 215.5; DB 20; Length 32.2%; Pred. No. 2.6e-15; tive 34; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Length 179;
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                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                             Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1999;
17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200073502-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbial infection; antibacterial; Helicobacter pylori infection;
                                                                                                                                                                                                                                                                                                                                                     Claim 37; Page 253; 366pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF25593
                                                                                                                                                                                                                                                                                                                                                                                                                                      Apfel H, Fuchs TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-2000; 2000WO-EP05024.
                                                                                                                                                                                                                                                                                                                                                                      essential genes in defective mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      2001-049948/06
122 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 175
                 117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                          15 SYLTEM-----TGCANKSTSQVMVAP-NAPTGYTGVIYT------GVAPLVDND 56
                                    65 PAVE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                     57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                         5 SVFSFLVAFLLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                       Similarity
                                                                                                                                                   179 AA;
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99DE-1027740
99DE-1034029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99DE-1024965
                                                                                                                      25.0%; Score 215.5; DB 22; Length 179; 32.2%; Pred. No. 2.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gibbs CP,
                                                                                                               34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hueck CJ,
                                                                                                               63;
                                                                                                                 Indels
                                                                                                                 21;
                                                                                                                 Gaps
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RESULT 15 AAW20795

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                                                                                                                                                                                                                                                                                                                                    This sequence is a H. pylori outer membrane protein.

C The protein may be used in a vaccine to prevent or treat H. pylori confection or to identify H. pylori polypeptide binding compounds, cusful as potential H. pylori life cycle activators or inhibitors. C overlapping contigs generated by mechanically shearing the bacterial control of the predicted coding regions defined by computer evaluation. To condity likely H. pylori antigens for vaccine development, the amino call sequences predicted from various oRF were analysed for significant cand determined the sequences of interest, particular regions can be considered from H. pylori by PCR amplification for recombinant polypeptide yr
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                        Query Match
AAW89813 standard; Protein; 179 AA.
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 56; Page 1203; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT68048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9640893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori outer membrane protein 07gp31516orf4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW20795 standard; Protein; 187 AA.
                                                                                                                                                                                                                                                                           Local Similarity
                                                                  130 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVQKTRECYRENRRVDV 183
                                                                                             117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                           73 PAIE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                      57 ETVKALASKLPSLVYFDFDSDETKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                    13 SVFSFLVAFLLVVGCSHKMDNKTVAGDVSTKAVQTAPVTTEPAPEKEEPKQEPAPVVEEK 72
                                                                                                                                                                                                                15 SVLIFM-----TGCANK------STSQVMVAP--NAPTGYTGVIYTGVAPLVDND 56
                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                    187 AA;
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0487032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0630405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US09122.
                                                                                                                                                                                                                                                                   25.0%; Score 215.5; DB 1 32.8%; Pred. No. 2.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mellgaerd BL;
                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                 DB 18;
                                                                                                                                                                                                                                                   66; Indels
                                                                                                                                                                                                                                                                              Length 187;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                          Query Match
           23-JAN-1998
                                                              AAW23592 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting antised that persists even after antimicriobial treatment. In highly sensitive and specific. The specification also describes 69 are used to detect H. pylori-specific cluster families. H. pylori antigens infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 96-97; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV90545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; immunogenic cluster family: vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by clone Gla ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW89813;
                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                              118 MSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                 123 QALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 175
                                                                                                                                                                                           64 KPAIESGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEANTDEFGSSEYN
                                                                                                                                                                                                                      66 LPSL------VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYN 117
                                                                                                                                                                                                                                                     4 SSAFSFLVAFLLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEE 63
                                                                                                                                                                                                                                                                                 8 AAAAAALSVLTFMTGCANKSTSQVMVAP-NAPTGYTGVIYTGVAPLVDNDETVKA-LASK 65
                                                                                                                                                                                                                                                                                                                          54; Conservative
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fry KE, Lim MY, McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                     179 AA;
      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0045107
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                                                                                                                                                                                                                                                                                                                                  24.6%; Score 211.5; DB 20; Length 179; 31.2%; Pred. No. 7.2e-15;
                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                        Mismatches
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hes 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omp22 gene; outer membrane protein; antigen; immunogen; stomach; gastritis; peptic ulcers; gastric cancer; diagnostic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09728264-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents Omp22, an outer membrane protein which exhibits antigenicity and immunogenicity against Helicobacter pylori. This bacterium is associated with inflammation of the stomach and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori outer membrane protein, Omp22 - used in a vaccine for treatment or prevention of H. pylori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastritis related diseases e.g. peptic ulcers and gastric cancer. Omp22 could be used in immunological therapy as a H. Pylori-specific antigen for the treatment and prevention of diseases associated with this microorganism e.g. as the active ingredient in a diagnostic kit or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT74195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-402617/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 5; 38pp; English.
Omp22 gene; outer membrane protein; antigen; immunogen; stomach;
                             H. pylori recombinant Omp22 recombinant outer membrane protein.
                                                          23-JAN-1998
                                                                                     AAW23591;
                                                                                                                    AAW23591 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                         127 VKRTLSVKNALVIKGVEKDMIKTISFGETKPKCTQKTRECYKENRRVDV 175
                                                                                                                                                                                                                     122 ERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                          62 LASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLG 121
                                                                                                                                                                                                                                                                                                       10 LVAFLFIAGCKHNMDKETVAGDVSAKAVQSAPVSTEIAQEKQEPKQEPAPVVEEKPAVE-
                                                                                                                                                                                                                                                                                                                                   14 LSVLTFMTGCANKSTSQVMVAP-NAPTGYTGVIYTGV-----APLVDNDETVKA 61
                                                                                                                                                                                                                                               69 -SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEYNQALG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moon H,
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96KR-0002105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Omp22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= leader_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= mature_peptide
                                                                                                                                                                                                                                                                                                                                                                              24.2%; Score 208.5;
30.8%; Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                      144 AA
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 1.5e-14
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                                                                                                                                                                                                                                                                                                                                                                                                DB 18; Length 179;
                                                                                                                                                                                                                                                                                                                                                                      69; Indels 15;
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sinusitis;

purulent otitis media; erythema nodosum; pharyngitis;

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RESULT 19
AAY35412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This amino acid sequence of Omp22, is a recombinant outer membrane protein which is identical to the mature protein of its native form (see AAW23592). It retains antigenicity and immunogenicity against Helicobacter pylori. This recombinant Omp22 protein can be mass produced in via expression in E.coli DH5-Alpha cells. H. pylori is associated with inflammation of the stomach and gastritis related diseases e.g. with inflammation of the stomach and gastritis related diseases e.g. peptic ulcers and gastric cancer. The native and the recombinant form of Comp22 could be used in immunological therapy as a H. Pylori-specific antigen for the treatment and prevention of diseases associated with this microorganism e.g. as the active ingredient in a diagnostic kit or a prophylactic/therapeutic vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastritis; peptic ulcers; gastric cancer; diagnostic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9728264-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Pages 25; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori outer membrane protein, \mbox{Omp22} - used in a vaccine for treatment or prevention of H. pylori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT74194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-402617/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                               Chlamydia pneumoniae transmembrane protein sequence
                                                                                                                                                                                                     AAY35412 standard; Protein; 192 AA
Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                      AAY35412;
                                                                                                      13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 ERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                   170 L 170
                                                                                                                                                                                                                                                                                                                                 140 V 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 APLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                23 APVVEEKPAVE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moon H, Park Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seo W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 205.5; DB 18; Length 144; Pred. No. 2.4e-14;
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                                                                                               Omp P6 precursor; outer membrane protein; Chlamydia infection; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; atherosclerosis; asthma;
                20-DEC-2000; 2000WO-CA01534.
                                                        WO200146224-A2
                                                                          Chlamydia pneumoniae
                                                                                                                                        Chlamydia pneumoniae omp P6 precursor protein.
                                                                                              vaccine; antibiotic.
                                                                                                                                                             04-SEP-2001 (first entry)
                                                                                                                                                                                      AAE04322
                                                                                                                                                                                                     AAE04322 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                    AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitts and is thought to be a contributing factor in heart nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in nucleotides sequences can also be used as immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 1196-1197; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357842/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; neutralising epitope.
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                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                          128
                                                                                                                                                                                                                                                                 111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                     68 DSKEEKQYKSSQVAAFRNITFATDSYTIKGEENLAILINLVHYMKKNPKATLYIEGHTDE 127
                                                                                                                                                                                                                                                                                                        54 DNDETVKALASKLPSL--VYFDFDSDEIK-PQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                RGAASYNLALGARRANAIKEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTE 186
                                                                                                                                                                                                                                                                                                                                                                          192 AA;
                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                                              23.8%; Score 204.5; DB 2 38.7%; Pred. No. 4.6e-14; tive 24; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                DB 20; Length 192;
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The present sequence is Chlamydia pneumoniae outer membrane protein (omp) P6 precursor. The omp P6 precursor polynucleotide, corpolypeptide and its antibody are useful for detecting, preventing and cut treating Chlamydia infections e.g. pneumonia, upper respiratory tract coresponding to the construction of the consociated with atherosclerosis and asthma. Immunogenic fragments corporated with atherosclerosis and asthma. Immunogenic fragments of the associated with atherosclerosis and asthma. Immunogenic fragments corporated corposition. The polynucleotide is useful in the construction of attenuated Chlamydia strains that can over express the polynucleotide or express it in a non-toxic, mutated form. The omp P6 probes are useful in diagnostic tests as capture or detection probes and the primers are cuseful in diagnostic methods involving PCR (polymerase chain reaction).
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Best Local :
03-JUL-2001; 2001WO-IB01445
                                                             10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke;
                                                                                                                       WO200202606-A2
                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                               strain CWL029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae cp7090 protein, SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murdin AD, Oomen RP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 RGAASYNLALGARRANAIKEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 DSKEEKQYKSSQVAAFRNITFATDSYTIKGEENLAILTNLVHYMKKNPKATLYIEGHTDE 127
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                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                        /note= "Mature protein"
                                                                                                                                                                                                                               /label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
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Best Local :
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11-JUL-2000;
21-JUL-2000;
07-AUG-2000;
18-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, anyocardial infarction, cerebrovascular disease, carotid artery stenosis, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in pcR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is pneumoniae is a common cause of respiratory disease in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 60; 364pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                          AAW89983 standard; Protein; 104 AA
                                  WO9849314-A2
                                                                     Helicobacter pylori
                                                                                                      peptic ulcer; gastric adenocarcinoma; gastric
                                                                                                              Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                              Expressed antigen for clone Y89A
                                                                                                                                                                                                       18-FEB-1999
                                                                                                                                                                                                                                          AAW89983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 DNDETVKALASKLPSL--VYFDFDSDEIK-PQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
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; 2000GB-0017047.
; 2000GB-0017983.
; 2000GB-0019368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AA;
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2000GB-0022583.
2000GB-0027549.
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                                                                                                                                                                                                       (first entry)
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
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25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 322; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENELABS TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                            04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                          paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis surface exposed protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY37603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY37603 standard; Protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                       W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis.
                                                                                                                                                                                                                                                 10-JUN-1999
   (GEST ) GENSET
                                                                                                                                                                                     27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEYNQALGVKRTLSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fry KE, Lim MY, McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US08487
                                                                                            98US-0107077.
97FR-0015041.
                                                                                                                                                                                           98WO-IB01939
                                                                     97FR-0016034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.9%; Score 197.5; DB 141.6%; Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 104;
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RESULT 24
AAB20105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                  Thonnard J;
                                                                        N-PSDB; AAF30043.
                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                         25-JUN-1999;
                                                                                                                                                                                                23-JUN-2000; 2000WO-EP05851.
                                                                                                                                                                                                                                                              WO200100836-A1.
                                                                                                                                                                                                                                                                                       Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                    BASB311; infection; otitis media; pneumonia; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20105 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                 antibacterial; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis BASB113 protein.
                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 1248-1249; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Griffais R;
                                                                                 2001-112458/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 HPVHPGHNELAWQQNRRTE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 RPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 VRHLHKSPKATLYIEGHTDERGAAAYNLALGARRANAVKQYLIKQGIAADRLFTISYGKE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 GFVPFYSDEEIQQAFVEDFDSKEEQLYKTSAQSTSFRNITFATDSYSIKGEDNLTILASL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 AA;
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                                                                                                                                                                     99GB-0015044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
23-AUG-2001
                                                          WO200161013-A1.
                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis;
                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression vectors, host cells and methods for producing BASBII3 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASBII3 polypeptide, or a polypeptide having at least polynucleotide encoding such a polypeptide. A claimed method of diagnosing a Moraxella infection involves identifying a BASBII3 polypeptide. A claimed method of polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection composition useful antibody directed against a BASBII3 polypeptide. BASBII3 and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOMP P5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB47447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB47447 standard; Protein; 353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of citis media in children and pneumonia in adults. The invention provides BASB113 polypeptides, and polynucleotides encoding them, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 67; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 QAAYNQELSERRADSVRYYLINQGVDPYRIQTVGYGMRQPIASNATEAGRAQNRRVEL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 SREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSONRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 VTHDTDTGNINLTMPGNITFAHDDDTLNSAFLGRLNQLANTMNQYHETTIVIVGHTDSTG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 VDNDETVKALASKLPSLYYFDFDSDETKPQAAAILDEQAQFLTTNQTARVLVAGHTDERG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 IGAVAGALGGTAISKATGGEKTGRDAIL-GAAVGAAAGAYMERQAKQIEQQMQGTGVT-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 IAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIY------TGVAPL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the state of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                             181..204
                                                                                                                                                                                                /label= Loop 3
/note=_"Extracellular domain"
                                                                                                                                                                                                                                                                        136..150
                                                                                                                                                                                                                                                                               /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                    /label= Loop 1
/note= "Extracellular domain"
                                                                                                           /note= "Extracellular domain'
                                                                                                                                            /label= Loop 4
                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            Гоор
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρy
FTT FTT STANKAR
                                                                                                                                                                                                                                                                                                                                                                            RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the major outer membrane protein P5 of non-typeable H. influenzae. One or more surface exposed loops of this protein may be replaced with a modified peptide of the invention. Each of these peptides contain an LB1(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP P5 from strain ntHill28, representing amino acids Argll7 to Gly135. This peptide represents the third exposed loop of P5 and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native of the invention are modified in terms of being in a non-native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2001; 2001WO-EP01556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       environment in the recombinant outer membrane protein. The modi MOMP P5 may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            otitis media and conjunctivitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-522599/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-2000; 2000GB-0003502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory tract infection.
                                                                                                                                                                            antibody; glutathione-S-transferase; GST
                                                                                                                                                                                              Vaccine; fusion protein; OprF; OprI; outer membrane protein;
                                                                                                                                                                                                                                 P. aeruginosa orpF-oprI fusion protein.
                                                                                                                                                                                                                                                                        01-OCT-1996
                                                                                                                                                                                                                                                                                                                                            AAR99626 standard; Protein;
                                   Protein
                                                                                        Protein
                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 QATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 PNTALNYNPWIGSINAGISYRFGQGAAPVVAAPEVVSKTFS-LNSDVTFAFGKANLKPQA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                   312 ATGYGKANPVTGATCDQVKGRKALIACFAPDRRVEIA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denoel P,
                                                                                                                                           aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                      (first entry)
                                  /label= oprF
/note= "oprF amino acids 192-342"
152..214
/note= "oprI amino acids 21-83"
                  /label= oprI
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%; Score 176.5; 30.6%; Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poolman J, Thonnard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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RESULT 27
AAR85450
                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein was expressed in Escherichia coli and Saccharomyces cerevisiae transformants. The oprF-oprI hybrid protein, and antibodies raised against it, conferred protection against p. acruginosa infection in laboratory animals. The hybrid protein was significantly more immunogenic than an oprI-oprF fusion (AAR99627).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A cDNA sequence (AAT32600) codes for a fusion (AAR99626) between amino acids 192-342 of the outer membrane protein F (oprF) and amino acids 21-83 of outer membrane protein I (oprI) of Pseudomonas aeruginosa ATCC 33354. A glutathione-S-transferase fusion with the hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 13-14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT32600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-279559/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Von Specht BU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broeker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion proteins for Pseudomonas aeruginosa vaccines - contgragments of outer membrane proteins I and {\bf F}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragments of outer membrane proteins I and
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                           AAR85450;
                                                                                                                                                                                                                                                                                                                      AAR85450 standard; Protein; 338
                                                                                                                                                                                                                                      Nontypable H. influenzae P5 protein.
                                                                                                                                                                                                                                                               15-FEB-1996
08-NOV-1995
                           EP680765-A1
                                                                                Misc-difference 311
                                                                                                                                                                 Haemophilus influenzae
                                                                                                                                                                                            chronic pulmonary obstructive disease
                                                                                                                                                                                                          P5 outer membrane protein; vaccine; otitis media; sinusitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                         111 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVESSH 154
                                                                                                                                                                                                                                                                                                                                                                                                                  130 NYLLGK-GINOASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                              51 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domdey H,
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94EP-0120023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95EP-0118098
                                                                                              /note= "amino acid at identified in
                                                    /note= "amino acid at position 311 is not
    identified in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.4%; Score 175.5; DB 1 37.5%; Pred. No. 7.8e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hungerer K, Knapp B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches
                                                                                                 position 195 is not
the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ulrich B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Novel isolated polynucleotide useful for producing fibronectin binding proteins which are useful in production of vaccine, in diagnostic assays and for prophylactic and therapeutic purposes
                                                                WPI; 2001-079546/09.
                                                                                           Garvis SG,
                                                                                                              (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                            16-MAY-1997;
                                                                                                                                                                                                 05-DEC-2000
                                                                                                                                                                                                                         US6156546-A
                                                                                                                                                                        15-MAY-1998;
                                                                                                                                                                                                                                                 Pseudomonas fluorescens
                                                                                                                                                                                                                                                                 Fibronectin binding protein; CadF; vaccine; diagnostic assay.
                                                                                                                                                                                                                                                                                              Protein associated with C.coli and C.jejuni CadF.
                                                                                                                                                                                                                                                                                                                                22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                            AAB59180;
                                                                                                                                                                                                                                                                                                                                                                           AAB59180 standard; protein; 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nontypable H. influenzae HI outer membrane protein P5 was isolated by extraction of the outer membrane with detergents and cation-exchange chromatography. P5 (or its peptide fragments) are used in vaccines for prevention of H. influenzae infections implicated in otitis media, sinusitis and chronic pulmonary obstructive disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 7-8; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purified H.influenzae P5 outer membrane protein - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preventing reducing susceptibility to or treating H.influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-375029/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMCY ) AMERICAN CYANAMID CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         295 ISATGYGKANPVTGATXDQVWGRWALIATLAPDRRVEIA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 VEIISFGEERPIAFGTNEEAWSQ-----NRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 QAQATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 INPNTAIHYNPXIGSINAGISYRFGQGAAP------VKTFSLNLD--VTFAFGKANLKP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 QAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQAS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 VAPNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                         Konkel ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                           97US-0046763.
                                                                                                                                                                    98US-0080025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0210394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95EP-0302996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%; Score 174.5; DB 16; Length 338; 28.9%; Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
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AAR99625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                          A cDNA sequence (AAT32599) codes for the C-terminal region, amino acids 190-350 (AAR99625), of the Pseudomonas aeruginosa ATCC 33354 outer membrane protein F (oprF). A hybrid protein between glutathione-S-transferase and the oprF moiety was expressed in Escherichia coli. oprF-oprI (AAR99626) and OprI-oprF (AAR99627) fusion proteins were also prepd. and tested for their efficacy as vaccines
 Sequence
                       proteins were also prepd. and te against P. aeruginosa infection.
                                                                                                                                      Disclosure; Page 11-12; 23pp; English.
                                                                                                                                                                               Fusion proteins for Pseudomonas aeruginosa vaccines - contg
                                                                                                                                                                                                                                   WPI; 1996-279559/29.
                                                                                                                                                                                                                                                                              Broeker M,
                                                                                                                                                                 fragments of outer membrane proteins I and {	t F.}
                                                                                                                                                                                                                      N-PSDB; AAT32599
                                                                                                                                                                                                                                                                  Von Specht BU;
                                                                                                                                                                                                                                                                                                                                       16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1995;
                                                                                                                                                                                                                                                                                                         (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                             EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; glutathione-S-transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; fusion protein; OprF; OprI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P. aeruginosa oprf C-terminal region (aa190-350).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR99625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campylobacter coli fibronectin binding protein (CddF). A recombinant expression vector with cadf is useful in an assay for determining the presence of C.jejuni or C.coli in a test sample or for determining whether a test isolate of Campylobacter is a strain of C.coli cadf is useful in the construction of DNA probes for identifying and quantifying the level of expression of Cadf in a cell. The gene can also be used in a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR99625 standard; Protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a Campylobacter jejuni or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 39-42; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 QVLVKDGVAPSRITAVGYGESRPVADNATEAGRAVNRRVEAS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 VKFDFDKSVVKPNSYGDVKNLADFMAQYPATNVEVAGHTDSIGPDAYNQKLSQRRADRVK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
161 AA;
                                                                                                                                                                                                                                                                          Domdey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                       94EP-0120023
                                                                                                                                                                                                                                                                                                                                                                 95EP-0118098
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                                                                                                                                                                                                                                                                          Hungerer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
                                                                                                                                                                                                                                                                        Knapp B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                     Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 326;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                     Query Match
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR99627 standard; Protein; 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR99627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; fusion protein; OprF; OprI; outer membrane protein;
antibody; glutathione-S-transferase; GST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. aeruginosa orpI-oprF fusion protein.
                                                                        A cDNA sequence (AAT34419) codes for a fusion (AAR99627) between amino acids 21-83 of the outer membrane protein I (oprI) and C-terminal amino acids 190-350 of outer membrane protein F (oprF) of Pseudomonas aeruginosa AFCC 3354, the 2 moieties being joined by a linker dipeptide. A glutathione-S-transferase fusion with the hybrid protein was expressed in Escherichia coll and Saccharomyces cerevislae transformants. The oprI-oprF hybrid protein was significantly less immunogenic than an oprF-oprI fusion (AAR99627).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1995;
                                                                                                                                                                                                                             Fusion proteins for Pseudomonas aeruginosa vaccines - contg. fragments of outer membrane proteins I and F.
                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1994;
                                                  Sequence
                                                                                                                                                                                                   Disclosure; Page 13-14; 23pp; English.
                                                                                                                                                                                                                                                                                                                           Broeker M,
                                                                                                                                                                                                                                                                                                                                                     (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                   1996-279559/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
38;
                                                                                                                                                                                                                                                                       AAT34419
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                    226 AA;
                                                                                                                                                                                                                                                                                                                          Domdey H,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                  94EP-0120023
                                                                                                                                                                                                                                                                                                                                                                                                            95EP-0118098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= OprI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "oprF amino acids 190-350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "oprI amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%;
             19.9%; Score 171.5; 37.6%; Pred. No. 2.3
                                                                                                                                                                                                                                                                                                                             Hungerer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OprF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 171.5; DB 1
pred. No. 1.4e-10;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                Knapp B,
              2.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Indels
                           DB 17; Length 226;
                                                                                                                                                                                                                                                                                                                                 Ulrich B;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ,
    1;
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     Gaps
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RESULT 31
B
                               QΥ
                                                                  B
                                                                                                 QΥ
                                                                                                                                       Matches
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                 The protein is isolated from the OMP of P. aeruginosa serotype 6 ATTC 33354) and purified by HPLC. The amino-terminal and trypsin fragments are sequenced and a series of oligonucleotide probes constructed corresponding to the established sequences. These probes are used to screen a gene bank of 15-20 kb fragments of genomic DNA in lambda EMBL 3. One positive clone includes a 15 kb insert contg. the protein gene, which can be isolated as a 2.5 kb PstI fragment. This fragment cannot be cloned int a high copy no. vector because of the toxicity of the gene prod.., so is subcloned as two fragments with an overlapping region of about 500bp. Ab's are raised by usual immunisation or cell-fusion procedures. The Ab's are useful in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP82053 standard; protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein F; OMPF; vaccination; antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane protein F of Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP82053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New outer membrane protein {\bf F} of Pseudomonas aeruginosa DNA sequences encoding it and derived antibodies, usefu vaccination and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE3718591-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; ; p; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1988-361619/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domdey H, Lottspeich F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAN82023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                        Sequence
                                                                                                                                                    Match 19.9%; Score 171.5; DB 9; Local Similarity 37.6%; Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                               130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                  242 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR
302 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 342
                                                                                                   70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                         38;
                                                                                                                                                                                                             350 AA;
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87DE-3718591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87DE-3718591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           von Specht B-U,
                                                                                                                                             15;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duchene M;
                                                                                                                                               47;
                                                                                                                                                  Indels
                                                                                                                                                                                Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for
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RESULT 33
AAY96098
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                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                   Actinobacillus pleuropneumoniae
                                          dual immune response; immunogen; pleuropneumonia.
                                                       Outer membrane protein; OmpAl; vaccine; pig; immunogen;
                                                                                      Actinobacillus pleuropneumoniae OmpA2.
EP1035133-A2
                                                                                                                   19-DEC-2000 (first entry)
                                                                                                                                                     AAY96098;
                                                                                                                                                                      AAY96098 standard; Protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              determining whether a test isolate of Campylobacter is a strain of C.coli. cadf is useful in the construction of DNA probes for identifying and quantifying the level of expression of Cadf in a cell. The gene can also be used in a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a Campylobacter jejuni or Campylobacter coli fibronectin binding protein (CadF). A recombinant expression vector with cadF is useful in an assay for determining the presence of C.jejuni or C.coli in a test sample or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated polynucleotide useful for producing fibronectin binding proteins which are useful in production of vaccine, in diagnostic assays and for prophylactic and therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 37-40; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-079546/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garvis SG, Konkel ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibronectin binding protein; CadF; vaccine; diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6156546-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein associated with C.coli and C.jejuni Cadf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB59179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB59179 standard; protein; 350 AA
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                     302 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 342
                                                                                                                                                                                                                                                                130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                       242 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 301
                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0046763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0080025.
                                                                                                                                                                                                                                                                                                                                                              19.9%; Score 171.5; DB 22; Length 350; 37.6%; Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Actinobacillus pleuropneumoniae strain Pz420
                               OmpA2; outer membrane protein; APP; pneumonic pathogen; swine; Sus scrofa; serotype; antigen; vaccine; cross-reactive immunity; cross-protection; diagnosis.
                                                                                                       Actinobacillus pleuropneumoniae outer membrane protein, OmpA2.
                                                                                                                                                        11-SEP-2000 (first entry)
                                                                                                                                                                                                 AAY97900;
                                                                                                                                                                                                                              AAY97900 standard; Protein; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vertebrate; and a second protein, which is an immunogen from a pathogen capable of infecting the vertebrate, and which causes the vertebrate's immune system to recognise the first protein, producing a response that inhibits the activity of the first protein, and also protecting the vertebrate from infection by the pathogen when the vertebrate is vaccinated with the fusion protein. In the present case, a fusion protein of cholecystokinin and Omph2 providing a protective immune response against porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae. OmpA2 can be utilised in fusion proteins of the invention that are used as vaccines eliciting a dual immune response. Such fusion proteins comprise: a first protein that is endogenous to a vertebrate, the activity of which is to be inhibited within the vertebrate, and which is incapable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 58-60; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              itself of eliciting an effective immunoinhibitory response in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of outer membrane protein OmpA2 of Actinobacillus pleuropneumoniae. OmpA2 can be utilised in fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fusion protein for producing a dual immune response comprises a peptide analogous to an endogenous peptide which is to be inhibited, connected to a peptide analogous to an immunogen from a pathogen which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infects a vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-566924/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2000; 2000EP-0301103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                      327 YGEANPVTGATCDKV--KGRKA 346
                                                                                                                                                                                                                                                                                                                                                       147 FGEERPIAFGTNEEAWSONRRA 168
                                                                                                                                                                                                                                                                                                                                                                                  267 AANTEIANLGLATPAIQVNGYTDRIGKEASNLKLSQRRAETVANYLVSKGQNPANVTAVG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 APDIHSVTAGLSYRFGQGAVAPVVEPEVVTKNFA--FSSDVLFDFGKSSLKPAAATALD-
                                                                                                                                                                                                                                                                                                                                                                                                                    90 QAQFLTTN----QTARVLYAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIIS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 APNAPTGYTGVIYT----GVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martinod SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0120454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.7%; Score 170; DB 21; Length 369; 34.5%; Pred. No. 6.6e-10; rative 20; Mismatches 61; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Durtschi BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yule TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 12;
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                                                                                                                                         AAB44589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a low molecular weight outer membrane protein, OmpA2, from Actinobacillus pleuropneumoniae (APP) strain Pz420 (ATCC 98930). The invention relates to the novel APP outer peach of the proteins Omp20, OmpW, Omp27, OmpA1 and OmpA2 (AAY97896-Y97900) and to nucleic acids encoding them (AAA38554-A38558). APP is a Gram negative coccobacillus which is one of the most important swine pneumonic pathogens. 12 different serotypes of APP have been recognised which vary in geographic distribution. Prior art attempts at vaccinating artists the property of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1001025-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           against App have produced mainly serotype-specific immune responses. In contrast, natural immunity to any one serotype seems to confer significant protection from disease caused by other serotypes, suggesting that natural exposure induces cross-reactive immunity to shared antiqens. The novel outer membrane proteins of the invention are present in all 12 serotypes, and may provide a target for cross-protective immunisation. The novel outer membrane proteins and nucleic acids encoding them can be used as a vaccine against App in swine. They can also be used as reagents for the diagnosis of App infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 5; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA encoding them, for use as vaccines against the bacteria in swine \mbox{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA38558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ankenbauer RG, Bawarren-Stewart LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Virulence gene protein #69
                                         08-FEB-2001 (first entry)
                                                                                AAB44589
                                                                                                                        AAB44589 standard; Protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-320438/28.
                                                                                                                                                                                                                                                                                                         267 AANTEIANLGLATPAIQVNGYTDRIGKEASNLKLSQRRAETVANYLVSKGQNPANVTAVG 326
                                                                                                                                                                                                                                                                                                                                                                                          210 APDIHSYTAGLSYRFGOGAVAPVVEPEVVTKNFA--FSSDVLFDFGKSSLKPAAATALD- 266
                                                                                                                                                                                                                             327 YGEANPYTGATCDKV--KGRKA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                    34 APNAPTGYTGVIYT----GVAPLVDNDETVKALASKLPSLYYFDFDSDEIKPQAAAILDE 89
                                                                                                                                                                                                                                                                                                                                                   QAQFLTTN---QTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIIS 146
                                                                                                                                                                                                                                                                    FGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-0308262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Signal peptide"
20..369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baarsch MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suiter BT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.7%; Score 170; DB 21; 34.5%; Pred. No. 6.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mature OmpA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keich RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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AAR66294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000; 2000WO-US09218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and bacterial infections such as septicemias, bronchopneumonias, rhinitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC79664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-647422/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowery DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHAA ) PHARMACIA & UPJOHN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 39; Pages 308-309; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wound infections.
              Region
                                                                                                     Haemophilus influenza strain 1128
                                                                                                                                                    Fimbrin protein; vaccine; otitis media.
                                                                                                                                                                                                           Non-typable Haemophilus influenza (NTHi) fimbrin protein
                                                                                                                                                                                                                                                                     09-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                            AAR66294;
                                                                                                                                                                                                                                                                                                                                                                              AAR66294 standard; Protein;
                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 APDIHSVTAGLSYRFGQGAVAPVVEPEVVTKNFA--FSSDVLFDFGKSSLKPAAATALD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 FGEERPIAFGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 AANTEIANLGLATPAIQVNGYTDRIGKEASNLKLSQRRAETVANYLVSKGQNPANVTAVG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 YGEANPVTGAT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 APNAPTGYTGVIYT----GVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 QAQFLTTN---QTARVLYAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIIS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fuller TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9905-0153453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0128689
                                                    Location/Qualifiers
/label= amino terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.6%; Score 169; DB 21; 35.9%; Pred. No. 8.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kennedy MJ;
                                                                                                                                                                                                                                                                                                                                                                                         359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 10;
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                                                                                                                                                                               RESULT 37
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                                                                                                                                                                                                                                                                                                                                   Matches
                                                       Moraxella; vaccine; respiratory tract infection; antiinflammatory; auditory; antibacterial; otitis media; sinusitis; pneumonia.
       07-MAR-2002
                                                                                        M catarrhalis MCA100854 protein SEQ ID NO:
                         WO200218595-A2
                                                                                                               19-JUL-2002 (first entry)
                                             Moraxella catarrhalis
                                                                                                                                      AAO17571;
                                                                                                                                                    AAO17571 standard; Protein; 228 AA
                                                                                                                                                                                                                                                                                                                                                                               influenzae 1128 strain is a particularly suitable immunogen to protect against the different non-typable HJ. influenzae that cause otitis media. Fimbrin protein is produced by culturing a transformed microbial host, pref. E.ocli, Sporodoptera frugiperda or a mucosal pathogen. Fimbrin protein (FP) produced by this process is claimed. The FP protein migrates in polyacrylamide genes to a posn. equiv. to a mool. wt. of 25.5 kD or 37.5 kD.
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The fimbrin proteins from 15 randomly selected type b and non-typable clinical isolates of Haemophilus influenzae share common
                                                                                                                                                                                                                                                                                                                                                                                                                                                       epitopes. Thus frimbrin isolated from non-typable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 5; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-006359/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OHIO-) OHIO STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9426304-A
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                    318 ATGYGEANPVTGATCDQVKGRKALIACLAPDRRVEIA 354
                                                                                                                                                                                                                       144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171
                                                                                                                                                                                                                                       258 QATILDSVYGEISQVKSRKVAVAGYTNRIGSDAFNVKLSQERADSVANVFVAKGVAADAIS 317
                                                                                                                                                                                                                                                                             199 PNTAINYNPWIGCINAGISYRFGQGEAPVVAAPEMVSKTES-LNSDVTFAFGKANLKPQA 257
                                                                                                                                                                                                                                                         84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                 35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ78916
                                                                                                                                                                                                                                                                                                                                                                       359 AA;
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kolattukudy PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0065442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US05477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= internal CNBr fragment
                                                                                                                                                                                                                                                                                                                                   19.2%; Score 165.5; DB 29.9%; Pred. No. 2e-09;
                                                                                                                                                                                                                                                                                                                           26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sirakova T;
                                                                                          22.
                                                                                                                                                                                                                                                                                                                                            DB 16; Length 359;
                                                                                                                                                                                                                                                                                                                        63; Indels 21;
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AAM50718
                                                                            RESULT 38
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                          AAM50718 standard; Protein; 344 AA.
AAM50718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can cause otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 28; Fig 21; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAL46503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-401721/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loosmore S, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AVET ) AVENTIS PASTEUR LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2001; 2001WO-CA01221.
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                      186 VASNATEOGREONRRIE 202
                                                                                                                                                                            153 IAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                         126 KLKAVPETTLRIIGHTDTQGTHEYNQDLSESRAAAVKEYLVSKGVAAERLNTQGASFDYP
                                                                                                                                                                                                                                               93 FLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERP 152
                                                                                                                                                                                                                                                                                       68 VADSIETARVAIVALG--DTVEENEMDILINALNTQIINFALDSTEIPQENKEILDLAAE
                                                                                                                                                                                                                                                                                                                                  33 VAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQ 92
                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-228295P
2000US-228439P
2000US-228440P
2000US-228441P
2000US-228442P
2000US-228443P
2000US-228443P
2000US-228443P
2000US-228512P
2000US-228712P
2000US-228773P
2000US-229474P
2000US-229404P
2000US-229404P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-229811P
                                                                                                                                                                                                                                                                                                                                                                               19.2%; Score 165; DB 23; 30.7%; Pred. No. 1.2e-09; 77. Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bradley B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ochs M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 228;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                               2;
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The present sequence is that of the HagA haemagglutinin of Haemophilus paragallinarum strain 2403 (serovar A), the causative agent of infectious coryza in chickens. The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and recombinant haemagglutinin polypeptides (see AAM50716-27) and coryza of chickens. The polypeptides are useful in vaccines for coryza of chickens. The polypeptides are useful in vaccines for memunisation against infectious coryza, as are the nucleic acids when expressed in attenuated bacteria, especially Salmonella or Mycoplasma (claimed). The recombinant polypeptide is preferably the mature protein, or a biologically active fragment, variant or derivative, that is capable of eliciting an immune response, in reviding an immune response.
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus paragallinarum strain 2403 haemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemagglutinin; HagA; antigen; vaccine; immunisation; coryza;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus paragallinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-2000; 2000AU-0008652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-2001; 2001WO-AU00822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABA91419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-154917/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terry TD, Tseng H, Hobb RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                 diagnosis of infectious coryza in chickens
                                                                                                                                                                                                                                                                                                                 providing protection against one or more strains of H. paragallinarum in chickens. Also claimed are methods of using the haemagglutinin polypeptides and nucleic acids for detection and
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                      ocar
                               136 GINQASVEIISFGEERPIAFGTNE-----EAWSQNRRAELS 171
                                                                239 RPEAQNVLDGIYGEIAQL----KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSK 294
                                                                                                                                 181 GRVEKDGSRVDYTPSIGSVTAGLSYRFGQSAPVVEPKVVAKTFA--LNSDYTFAFGKANL 238
                                                                                                                                                                     22 GCANKSTSQVMVAPNAPTGYTGVIYT--GVAPLVDNDETVKALASKLPSLVYFDFDSDEI 79
                                                                                                80 KPQAAAILD----EQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK 135
                                                                                                                                                                                                        51;
                                                                                                                                                                                                                    h 18.8%; Score 161.5; DB 23; Length 344; Similarity 30.9%; Pred. No. 5.1e-09;
GVAQEVISSTGYGEANPVTGAKCDTVKGRKALIACLADDRRVEIS 339
                                                                                                                                                                                                                                                                         344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Mature_protein
                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jennings MP,
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Downes J;
                                                                                                                                                                                                             68;
                                                                                                                                                                                                                Indels
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239 RPEAQNVLDGIYGEIAQL----KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSK 294

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RESULT 39
AAM50721
                                                                                                                                                 The present sequence is that of the HagA haemagglutinin of CC agent of infectious coryza in chickens. The invention provides CC agent of infectious coryza in chickens. The invention provides CC encoding nucleic acids (see ABA91417-27) from 11 strains (serovars CC a, B and C) of H. paragallinarum, the causative agent of infectious CC immunisation against infectious coryza, as are the nucleic acids CC when expressed in attenuated bacteria, especially Salmonella or CC when expressed in attenuated bacteria, especially Salmonella or CC the mature protein, or a biologically active fragment, variant or CC derivative, that is capable of eliciting an immune response, derivative, that is capable of eliciting an immune response, coryza paragallinarum in chickens. Also claimed are methods of using the CC paragallinarum in chickens. Also claimed are methods of using the CC diagnosis of infectious coryza in chickens.
                                                          Ωy
                                뫄
                                                                                          Matches
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemagglutinin; HagA; antigen; vaccine; immunisation; coryza;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus paragallinarum strain 0222 haemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM50721 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus paragallinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM50721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABA91422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Terry TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000AU-0008652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-2001; 2001WO-AU00822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200204485-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-154917/20
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the species
                                                                                                                                                 Sequence
                                                                                                         Local
                                181 GRVEKDGSRVDYTPSIGSVTAGLSYRFGQSAPVVEPKVVAKTFA--LNSDVTFAFGKANL 238
80 KPQAAAILD----EQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK 135
                                                           22 GCANKSTSQVMVAPNAPTGYTGYIYT--GVAPLVDNDETVKALASKLPSLVYFDFDSDEI 79
                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tseng H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                    344 AA;
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hobb RI,
                                                                                                           18.8%;
                                                                                               25;
                                                                                                           Score 161.5; DB 2
Pred. No. 5.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jennings MP,
                                                                                                Mismatches
                                                                                                                             DB 23; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Downes
                                                                                                  68;
                                                                                                     Indels
                                                                                                     21;
                                                                                                      Gaps
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The present sequence is that of the HagA haemagglutinin of C Haemaphilus paragallinarum strain 2671 (serovar B), the causative agent of infectious coryza in chickens. The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and CC encoding nucleic acids (see ABA91417-27) from 11 strains (serovars CC encoding nucleic acids (see ABA91417-27) from 11 strains (serovars CC encoding nucleic acids (see ABA91417-27) from 11 strains (serovars CC encoding nucleic acids (see ABA91417-27) from 11 strains (serovars CC encoding nucleic acids (see ABA91417-27) from 12 strains (serovars CC encoding against infectious coryza, as are the nucleic acids (see ABA91417-27) from 13 strains of the mature protein, or a biologically active fragment, variant or CC encoding protection against one or more strains of the providing protection against one or more strains of the CC paragallinarum in chickens. Also claimed are methods of using the CC diagnosis of infectious coryza in chickens
                                                                                                    Query Match
Best Local :
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                       Sequence
                                                                                                                                                                         diagnosis of infectious coryza in chickens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by the species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Terry TD, Tseng H, Hobb RI, Jennings MP, Downes J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABA91423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-154917/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-2000; 2000AU-0008652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-2001; 2001WO-AU00822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200204485-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus paragallinarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus paragallinarum strain 2671 haemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemagglutinin; HagA; antigen; vaccine; immunisation; coryza;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM50722 standard; Protein; 344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM50722;
181 GRVEKDGSRVDYTPSIGSVTAGLSYRFGQSAPVVEPKVVAKTFA--LNSDVTFAFGKANL 238
                                22 GCANKSTSQVMVAPNAPTGYTGVIYT--GVAPLVDNDETVKALASKLPSLVYFDFDSDEI 79
                                                                             51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 GVAQEVISSTGYGEANPVTGAKCDTVKGRKALIACLADDRRVEIS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 GINQASVEIISFGEERPIAFGTNE------EAWSQNRRAELS 171
                                                                                                                                                   344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide 22..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                18.8%; Score 161.5; DB 23; Length 344; 30.9%; Pred. No. 5.1e-09; tive 25; Mismatches 68; Indels 21; Gaps
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밁 QΥ

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Search completed: July 6, 2003, 14:04:28
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                                                                                                                        239 RPEAQNVLDGIYGEIAQL----KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSK 294
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length: 2000000000
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172
1 MMLHIQIAAAAAAL
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  GenCore version 5.1.6 (c) 1993 - 2003 Compugen
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GSHI_MOUSE
PYRK_METKA
MTRC_METTH
MTRC_METTM
HXD8_HUMAN
HXD8_HUMAN
PSBO_CHLRE
RBSK_BACHD
GSH2_HUMAN
GSH2_MOUSE
GVPL_HALME
SLP1_DROME
A85B_MYCKA
GDC_BOVIN
RLAO_METUA
GUB_FIBSU
DKK3_HUMAN
KLF2_MOUSE
KLF2_HUMAN
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AZUP_PARPN
PAL_ECOLI
RBMS_XENLA
RBMS_CHICK
CTF1_MOUSE
RL14_RAT
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Q60753
Q63507
Q10672
P31315
Q9ubp4
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Q9bzm3
P31316
Q02237
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P21160
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P54049
P17989
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027229
P80185
P13378
P12853
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P80401
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P39844
P20105
P02733
P20617
P04002
P80515
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                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                   3 legionella
4 bacillus su
5 drosophila
3 pseudopleur
7 myoxocephal
2 pseudopleur
5 araneus dia
7 araneus dia
                                                              7 rattus norv
2 mycobacteri
5 mus musculu
7 methanopyru
9 methanobact
5 methanobact
6 methanobact
8 homo sapien
3 chlamydomon
1 bacillus ha
3 homo sapien
6 mus musculu
halobacteri
                                                                                                                                                            xenopus lae
l gallus gall
mus musculu
homo sapien
mus musculu
homo sapien
                                               drosophila
mycobacteri
                                                                                                                                                                                     paracoccus
escherichia
                        methanococc
fibrobacter
                                        bos taurus
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RESULT

ALIGNMENTS

FSH_DROME
HMCU_DROME
EDD_HUMAN
ANP3_MYOSC
ANP5_MYOAE
ANP8_MYOSC
RL40_YEAST
RL40_YEAST
RL40_YEAST
RL40_TOBAC
SR14_MACRA
ANP4_PSEAM

0903	0783	91a9 2808	4647	0273 2046	1886	8004	4090	0436 1479	2042	9507 0436	1018	91en 1370	9uqb3	38054	24432	15139	17851	2153	0520	3870	2281	1305	0000	0701	0294	0753	5252	2184	3767	3329 2511	1797	1350	3558 5272	000	) uju 2475	382	380	1447	488	2417 5021	P42253	603
imanda	seudople	ibrio pr	erichi	seudopleu	icotia lacaca	custa mi	ryptococc	ocepha haromy	yoxocepha	omo sapie voxocepha	rosophila	hlamydomo rosophila	sapie	leri	ophila	Sa	orhabd	accha	rosop	accha	rosop	rosop	canis famil	scher	salmonella escherichia	os ta	nn s	ypan	scher	fa Y	mo sapie	mo sapie	mesocricetu rattus norv	mo sapie	sapie ophila	o sapie	reptomyc	robacter	scaris su	ryza sati omo sapie	cillus	esocrioet es

YCBU_BACSU
FL_ORYSA
HB9_HUMAN
HUMA_ASCSU
RL4_HUMAN
HUMA_ASCSU
RL4_HUMAN
TUD4_AGRVI
MUFF_STRTO
EVX2_HUMAN
TUD4_AGRVI
MUFF_STRTO
EVX2_HUMAN
TUD4_AGRVI
MUFF_STRTO
EVX2_HUMAN
TUD4_AGRVI
MUFF_STRTO
EVX2_HUMAN
WARAI_MESAI
MAB1_HUMAN
WARAI_MESAI
NAB1_HUMAN
WAB1_KIMAN
BAF1_KLUMA
CALR_PIG
LYXK_ECOLI
TGR1_HUMAN
VSM5_TRYBR
ZIC2_HUMAN
WSM5_TRYBR
ZIC2_HUMAN
WSM5_TRYBR
ZIC2_HUMAN
WSM5_TRYBR
ZIC2_MOUSE
ZIC2_HUMAN
WSM5_TRYBR
ZIC2_MOUSE
ZIC2_MOUSE
ZIC2_BORGE
ZIC2_BORGE
ZIC2_CALEE
ZIC2_CALEE
ZIC2_CAREE
LHMCC_DROME
ZIC2_CAREE
LHMCC_DROME
LIZ3_CAEEL
HMCC_DROME
LIZ3_CAEEL
HMCC_DROME
LIZ3_CAEEL
HMCC_DROME
ZYBR_CAEEL
HMCC_BROME
YBYK_CAEEL
LHMCN_MOUSE
OMB_DROME
YBYK_CAEEL
CUSA_ECOLI
DOLL
RETTH
CTD2_HUMAN
WRC2_CHLRE
OMB_DROME
CUSA_ECOLI
DOLL
RETTH
CTD2_HUMAN
WACC_CHLRE

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RESULT 2
PBP_BACSU
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Best Local
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                                                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
             01-FEB-1995
01-FEB-1995
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                                                P39844;
                                                                   PBP_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1. PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60543; CAA43033.1; -. PIR; A60337; A60337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legionella pneumophila.";
Infect. Immun. 59:2515-2521(1991).
-i- FUNCTION: VERY STRONGLY ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91310296; PubMed=1855972;
Ludwig B., Schmid A., Marre R., Hacker J.;
"Cloning, genetic analysis, and nucleotide sequence of a determinant coding for a 19-kilodalton peptidoglycan-associated protein (Ppl) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engleberg N.C., Howe D.C., Rogers J.E., Arroyo J., "Characterization of a Legionella pneumophila gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen) (PF
PAL OR PPLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein; Outer membrane; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S16631; S16631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - I - SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipoprotein antigen.";
Mol. Microbiol. 5:2021-2029(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legionella pneumophila.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptidoglycan-associated lipoprotein precursor (19 kDa surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P26493;
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AA100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Attached
                                                                                                                                                        105 AGHTDERGSREYN 117
                                                                                                                                                                                                                             l Similarity
13; Conserv
                                                                                                                                                                             AGHTDERGSREYN 117
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                                                                                                                                                                                                                                                                                                104
176 AA;
           (Rel. 31, Created)
(Rel. 31, Last sequence update)
                                                                                                                                                                                                                             Conservative
                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                  18911 MW;
                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                             7.68;
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                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                          Score 13; DB 1;
Pred. No. 5.2e-
                                                                                                                                                                                                                                                                                                                                PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN.
N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                   OMPA-LIKE
                                                                 PRT;
                                                                                                                                                                                                                                                                                              7D9C3EBECBE621DB CRC64;
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                                                                 491 AA
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                                                                                                                                                                                                                                            .2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Legionellaceae group;
                                                                                                                                                                                                                                                           Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eisenstein B.I.; encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by a lipid
                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                         0;
             RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Honaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Satot T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Schiguchi A., Tacconi E., Takayi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassumoto K., Yata K.,
RA Winers P., Wipat A., Yamamoto H., Yamane K., Yoshikawa H., Danchin A.,
RA Yoshida K., Yoshikawa H.F., Zumsteln E., Yoshikawa H., Danchin A.,
RA Yoshida K., Yashikawa H.F., Zumsteln E., Yoshikawa H., Danchin B.
                                                                            PRINTS; PR00922; DADACBPTASE3.
TIGRFAMS; TIGR00666; PBP4; 1.
                                                                                                               MEROPS; $13.UPW; -.
SubtiList; BG10969; pbp.
InterPro; IPR000667; Peptidase_S13.
Pfam; PF02113; Peptidase_S13; 1.
                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
                           SIGNAL
                                            Complete proteome.
                                                           Peptidoglycan synthesis; Cell division; Cell wall; Hydrolase; Signal;
                                                                                                                                                                                      EMBL; Z99113; CAB13718.1;
                                                                                                                                                                                                       EMBL; 234883; CAA84366.1;
                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tognoni A., Franchi E., Magistrelli C., Colombo E., Cosmina P.,
Grandi G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last annotation update) Putative penicillin binding protein precursor PBP OR DACC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 141:645-648(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A putative new peptide synthase operon in Bacillus subtilis: partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95227362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
Bacteria; Firmicut
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY S13; ALSO KNOWN AS THE D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 3 FAMILY.
                                                                                                                                                                     S13.UPW;
                                                                                                                                                                                                                                                                                           non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=7711903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillales; Bacillaceae;
POTENTIAL.
PUTATIVE PENICILLIN BINDING PROTEIN
                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                          Usage
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RESULT 3

ID 474A_DROME
ID 274A_DROME
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 15-JUN
DE ECGYSO
GN EIF74E
OC DINACOM
NCBIT
RN (I]
RP SEQUEN
RX MEDLIN
RA BUTLIS
RT Inducti
RL Cell 6
RN (21)
RP DEVELC
RX MEDLIN
RA Huet F
RT "Puffs
RT "Cell 6
RN (2-i- Si
CC -i- Si
CC -i- Ai
CC -i- Si
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                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Pfam; PF00178; Ets; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- SUBCELLULAR LOCATION: Nuclear.
-I- ALTERNATIVE PRODUCTS: 2 isoforms; A/E74A (shown here) and B/E74B
-(AC PIL1536); are produced by alternative splicing.
-I- DEVELOPMENTAL STAGE: In mid instar larvae salivary glands levels are low during puff stage 1 and increase during puff stage 2 to become the predominant form in stage 3. Levels reach maximum in late larvae during puff stages 8-10, decreasing abruptly at stage 11. This expression pattern is also seen in Malpidhian tubules and fat body. Transcripts are detected again in salivary glands from puff stages 12-14 and 17-21.
-INDUCTION: THE EXPRESSION OF THIS PROTEIN IS DEVELOPMENTALLY DECRIFACED.
            FlyBase; FBgn0000567; Eip74EF.
InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
                                                                                                          HSSP; P14921; 2STT.
TRANSFAC; T00208; -
                                                                                                                                                                 PIR; A34692; A34692.
                                                                                                                                                                                            EMBL; M37082; AAA28493.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ecdysone responses in Drosophila.";
Development 118:613-627(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Puffs and PCR: the in vivo dynamics of early gene expression during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94038699; PubMed=8223281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burtis K.C., Thummel C.S., Jones C.W., Karim F.D., Hogness D.S., "The Drosophila 74EF early puff contains E74, a complex ecdysone-inducible gene that encodes two ets-related proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 61:85-99(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE-90199900; Pubmed=2107982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ecdysone-induced protein 74EF isoform A (ETS-related protein E74A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P20105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATED AND IS CORRELATED WITH THE 20-OH-ECDYSONE INDUCED ACTIVITY OF PUFF 74EF.
SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AAAALSVL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AAAALSVL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richards G.;
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Best Local
                                               Antifreeze protein; Repeat; Multigene family. SEQUENCE 37 AA; 3144 MW; 46AA951A962DECA9 CRC64;
                                                                                                                                                                                                                             americanus).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
                                                                          PRINTS;
                                                                                                                                        Biochim. Biophys. Acta 495:388-392(1977).
                                                                                                                                                       Devries A.L., Lin \mathbf{Y}_{\cdot,i} antifreeze and mechanism of adsorption to
                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                      InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI
                                                                                                                                                                               MEDLINE=78060969; PubMed=588591;
Devries A.L., Lin Y.;
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                       Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                                                                                                                                                         Antifreeze peptide 3
                                                                                                                                                                                                                                                                                                                                                       P02733;
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SMART; SM00413; ETS; 1.

PROSITE; PS00345; ETS_DOMAIN_1; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS00346; ETS_DOMAIN_3; 1.

Nuclear protein; Transcription regulation; DNA-binding;

Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                     ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                 FUNCTION: ANTIFREEZE PROTEINS LOWER THE BLOOD SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY.
                                                                                                A03192; FDFL3W.
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        Similarity 7; Conserv
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8; Conserv
       Conservative
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  100.0%; F1
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100.0%; Pred. No.
              Score 7; I
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POLY-GLY.
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      Mismatches
              DB 1;
o. 6.2;
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                         Length 37;
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   Indels
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Gaps
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Best Local :
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Antifreeze peptide GS-8.

Myoxocephalus aenaeus (Grubby sculpin).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;

Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  grubby sculpin, Myoxocephalus aenaeus.";
Can. J. Zool. 66:403-408(1988).
-i- FUNCTION: ANTIFREEZE PROTEINS LOWER THE BLOOD FREEZING POINT-i- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANP8_MYOAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chakrabartty A., Hew C.-L., Shears M., Fletcher G.; "Primary structures of the alanine-rich antifreeze polypeptides from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8096;
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                                                                                                                                                                                                                                                                                                                            Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                                                                                                                                                                                           Antifreeze protein A/B precursor
                                                                                                                                                                                                                                                                                                                                                       23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             ANPA_PSEAM
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                                                                                                                                                                                SEQUENCE FROM N.A. (PROTEIN A).
MEDLINE-82197490; PubMed-6952188;
Davies P.L., Roach A.H., Hew C.-L
                                                                                            SEQUENCE FROM N.A. (PROTEIN A).
MEDLINE=88259236; PubMed=3133486;
                                                                                                                                                                                                                                          NCBI_TaxID=8265;
SEQUENCE FROM N.A. MEDLINE=84264559;
                                                    pleuronectinae.
                                                                    "Differential amplification of antifreeze protein
                                                                                 Scott G.K., Davies P.L., Kao M.H.,
                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 79:335-339(1982)
                                                                                                                                                                   DNA sequence coding for an antifreeze protein precursor from winter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL. S07046; FDF18G
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                                          Evol.
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Conservative (
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                                          27:29-35(1988).
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 . (PROTEIN B).
PubMed=6086629;
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                                                                                      Fletcher G.L.;
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                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Energy-optimized structure of antifreeze protein and its binding
                                                                                                                                                                                                                                                                                                                   EMBL; L00138; AAB59964.1; -.
EMBL; L29178; AAB59964.1; JOINED.
EMBL; M62414; AAA49469.1; -.
EMBL; X07506; CAA30389.1; -.
EMBL; M62416; AAA49471.1; -.
EMBL; M62417; AAA49472.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sicheri F., Yang D.S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95281060; PubMed=7760940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 45-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mechanism.
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                                                                                                                                                                                                                                                                                                      EMBL;
PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Ice-binding structure and mechanism of an antifreeze protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-STRUCTURE MODELING OF 45-81
                                                                                                     CONFLICT
HELIX
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                                                                                                                                         VARIANT
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                                                                                                                              VARIANT
                                                                                                                                                                                                                         interPro;
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                                                         Local
                                                                                                                                                                                                                                  1WFB; 03-JUN-95.
                                                                                                                                                                                                                                                                      JS0704; JS0704
                                                                                                                                                                                                                                                          1ATF; 15-OCT-94.
 50 AAAAAAL 56
                      8 AAAAAAL 14
                                                         Similarity
                                                                                                                                                                                                                         IPR000104; Antifreeze_1.
                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                03-JUN-95.
                                               Conservative
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36
70
24
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                                                                                              7711 MW;
                                                                                                                    82
36
70
24
                                                                                                                                                                                                    Repeat; Multigene family; Signal; 3D-structure.
                                                          4.1%; Score 7;
100.0%; Pred. No
                                                0;
                                                                                                                  A -> D (IN PROTEIN B).
S -> R (IN REF. 2).
                                                                                              C2AE7B74C0D46CC1 CRC64;
                                                                                                                                                     ANTIFREEZE PROTEIN A/B
                                                                                                                                                                             REMOVED BY A DIPEPTIDYLPEPTIDASE
                                                             Pred. No.
                                                                                                                                          A -> V
                                                Mismatches
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RESULT

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RESULT
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Best Local
                                                                                                            980517;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adult-specific rigid cuticular protein 12.6 (
                                                                            SEQUENCE
                                                                                            Structural protein; Cuticle. DOMAIN 73 83
                                                                                                                                                                                                                                                                 MEDLINE-97166616; PubMed-9014336;
NOTUP T., Berg T., Stenholm H., Andersen S.O., Hoejrup P.;
"Purification and characterization of five cuticular proteins
                                                                                                                                                                                                                                                                                                                                                                                    Araneus diadematus (Spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
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CU19_ARADI
P80515;
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Insect Biochem. Mol. Biol. 26:907-915(1996).
-!- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
-!- MASS SPECTROMETRY: MW-11872.1; METHOD-Electrospray.
-!- SIMILARITY: CONTAINS 1 CUTICLE CONSENSUS DOMAIN.
InterPro; IPR000618; Insect_cuticle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CU26_ARADI
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PROSITE; PS00233; CUTICLE; 1.
                                                                                                                                                                                                                                                                                                                               rISSUE=Cuticle;
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adult-specific rigid (Cular protein II.9 (ACP 11.9).
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=45920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norup T., Berg T., Stenholm H., Andersen S.O., Hoejrup P., "Purification and characterization of five cuticular proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97166616; PubMed=9014336;
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                        Local
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          Similarity 7; Conserv
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          Conservative
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       100.0%; F
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                 4.1%; Score 7; 1
100.0%; Pred. No.
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; 8D3E577C61999DC2 CRC64;
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                                                                     9BFBFCFB2B6AA4B9 CRC64;
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       Mismatches
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                   DB 1;
5. 18;
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                                   Length 127;
     0;
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     Indels
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THE THE PROPERTY OF A CONTROL OF THE PROPERTY OF THE
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AZUP_PARPN
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                              METAL
                                                               CHAIN
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P80401;
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                                                                                                                                            Copper; Electron transport; SIGNAL 1 22
                                                                                                                                                                                              Pfam; PF00127; copper-bind; 1.
PRINTS; PR00156; COPPERBLUE:
ProDom; PD001235; Copper_blue; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
                                                                                                                                                                                                                                                                                                          InterPro; IPR000923; BlueCu_1.
InterPro; IPR001235; Copper_blue.
                                                                                                                                                                                                                                                                                                                                                                       PDB; 1ADW; 15-MAY-97.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z73141; CAA97485.1; -. EMBL; Z70033; CAA93848.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: HOMODIMER.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1997) to the PDB data bank.

-!- FUNCTION: THIS SOLUBLE ELECTRON TRANSFER COPPER PROTEIN IS REQUIRED FOR THE INACTIVATION OF COPPER-CONTAINING NITRITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete amino acid sequence confirms the presence of pseudoazurin in Thiosphaera pantotropha."; Biochem. J. 308:585-590(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE=95289994; PubMed=7772045;
Chan C., Willis A.C., Robinson C.V., Aplin R.T., Radford S.E.,
Terguson S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 23-145.
STRAIN-ATCC 35512 / IMD 82.5;
MEDLINE-95289994; PubMed=7772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The pseudoazurin gene from Thiosphaera pantotropha: analysis of upstream putative regulatory sequences and overexpression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97184655; PubMed=9032456;
Leung Y.-C., Chan C., Reader J.S., Willis A.C., van Spanning R.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 23-32 STRAIN=ATCC 35512 / LMD 82.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paracoccus pantotrophus (Thiosphaera pantotropha).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli."
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15-JUL-1998 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferguson S.J., Radford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=82367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudoazurin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDUCTASE IN THE PRESENCE OF OXYGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 AAAAAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321:699-705(1997).
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36, Last sequence update)
41, Last annotation update)
           145
115
62
100
103
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PSEUDOAZURIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                             Signal; Periplasmic; 3D-structure.
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RESULT 10
PAL_ECOLI
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Best Local
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P07176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidoglycan-associated lipoprotein precurso
PAL OR EXCC OR B0741 OR Z0909 OR ECS0776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                       Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R., Piunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lazzaroni J.-C., Portalier R.;
"The excC gene of Escherichia coli K-12 required for cell envelope integrity encodes the peptidoglycan associated lipoprotein (PAL).";
Mol. Microbiol. 6:735-742(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
                                                                                                                           "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage matchine DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of the gene for t. lipoprotein of Escherichia coli K12."; Eur. J. Biochem. 163:73-77(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87133578; PubMed=3545827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562, 83334;
                                                              STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                          Sampei G.
                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                           ., Seki Y., Tagami H., Takemoto K., Wada C., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Henning U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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15446 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; ; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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; 725ECB5929EC3831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein precursor. OR ECS0776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for the peptidoglycan-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 145;
                                                                                                                                             linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
      Potamousis K.,
                                                                                                                                                                                          Yamamoto Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                            Saito N.
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Query Match
Best Local S
Matches 7
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"Crystallization and preliminary crystallographic study of the
peptidoglycan-associated lipoprotein from Escherichia coli.";
Acta Crystallogr. D 57:317-319(2001).
Acta Crystallogr. D 57:317-319(2001).
-i-FUNCTION: Thought to play a role in bacterial envelope integrity.
-i-SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
[6]
                                                                                                                                                                                                                                                                                                                                                                                                                                      entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apodaca J., Anantharaman T.S., Lin J., Yen G., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         their products, components of a multistep translocation system Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                DOMAIN
SEQUENCE
                                                                                              CHAIN
LIPID
                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levengood S.K., Webster R.E.;
"Nucleotide sequences of the tola and tolb genes and localization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90078104; PubMed=2687247;
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                                                                                                                                                             PRINTS; PRO1021; OMPADOMAIN.

PROSITE; PSO00013; BAC_OMPA; 1.

PROSITE; PS01068; OMPA; 1.

PROSITE; PS01068; OMPA; 1.
                                                                                                                                            Outer membrane; Signal; Lipoprotein; Complete proteome
                                                                                                                                                                                                                                            EcoGene; EG10684; pal
InterPro; IPR001145; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                SIGNAL
                                                                                                                                                                                                                               Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                              S20547; S20547
                                                                                                                                                                                                                                                                                          A27534; LPECPG.
                                                                                                                                                                                                                                                                                                         M28232; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                        AE000177; AAC738351; -. D90713; BAA35407.1; -. AE005252; AAG55077.1; -. AP002553; BAB34199.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         X05123; CAA28771.1; -. X65796; CAA46673.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          an email to license@isb-sib.ch).
                Similarity
                                                            22
22
105
173
   Conservative
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                                                                   AA;
                                                                                 22
149
                                                                   18824 MW;
                                                                                                                                                                                                                                                Bac_OmpA
                4.1%; Score 7;
100.0%; Pred. No
     0;
                                                                                  OMPA-LIKE
                                                                                                PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN N-ACYL DIGLYCERIDE.
                     Pred. No.
                                                                   449F9959C0274430 CRC64;
     Mismatches
                                   DB
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                                     Length 173;
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-!- FUNCTION: MAY BIND FINA.
-!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING HEART, PRONEPHROS,
RETINA AND EPIPHYSIS. IN ADULT, HIGH EXPRESSION IN HEARP, MODERATE
IN KIDNEY, UNDETECTABLE IN LIVER, LUNG AND SKELETAL MUSCLE.
-!- DEVELOPMENTAL STAGE: MENA FIRST DETECTED IN THE TALLBUD EMBRYO
(STAGE 26) IN THE PAIRED HEART PRIMORDIA AND IN THE CONDENSING
EPITHELIUM THAT WILL FORM THE PRONEPHROS; AT THE LATE TALLBUD
STAGE (STAGE 34) IN THE DEVELOPING RETINA AND EPITHYSIS. AS
DEVELOPMENT PROCEEDS, DETECTED THROUGH THE ENTIRE LENGTH OF THE
HEART TUBE, IN THE MUSCULAR TISSUE OF THE OUTFLOW TRACT, AND IN
THE DUCT EPITHELIUM OF THE PRONEPHROS. DURING LATER DEVELOPMENT,
MENA FOUND IN ALL SUBREGIONS OF THE HEART, IN THE GLOWUS, TUBULES
AND DUCT OF THE PRONEPHROS, IN THE RETINAL GANGLION CELL LAYER
AND DUCT OF THE PRONEPHROS, IN THE RETINAL GANGLION CELL LAYER
                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9YGF5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA-binding protein with multiple splicing homolog (RBP-MS) (HEart, RRM Expressed Sequence) (Hermes).
                                                                                                                                   SEQUENCE
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                          InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00350; RRW; 1.
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XENLA
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the developing heart.";
Mech. Dev. 80:77-86(1999).
                                                                                                                                                                                                                                                                                                    HSSP; P09012;
                                                                                                                                                                                                                                                                                                                  EMBL; AF107889; AAD16971.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerber W.V., Yatskievych T.A., Antin P.B., Correia K.M., Conlon R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99195799; PubMed=10096065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The RNA-binding protein gene, hermes, is expressed at high levels in the developing heart ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krieg P.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RBMS_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GCL) AND IN THE EPIPHYSIS. SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
167 AAAAAAI 173
                               œ
                                                                Similarity 7; Conserv
                                                                                                                                                                                                              PS00030; RRM_RNP_1;
                               AAAAAAL 14
                                                                                                                                                                                                                                 PS50102;
                                                                                                                                 167
196 AA;
                                                                Conservative
                                                                                                                                                                  20
11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                 RRM;
                                                                                                                                                 97
14
172
                                                                                                                               21675 MW;
                                                                              100.0%;
                                                                             4.1%; Score 7;
100.0%; Pred. No.
                                                                0;
                                                                                                                       POLY-ALA.
; 7964198C1122A3D3 CRC64;
                                                                                                                                                                 POLY-ASN.
                                                                                                                                                                               RNA-BINDING (RRM).
                                                                                                                                                                                                                FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                Mismatches
                                                                              DB 1;
o. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 AA
                                                                                              Length 196;
                                                               0;
                                                             Indels
                                                           0;
                                                           Gaps
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Вb
                                                                                                                                                                                                                                                                                                                                           CTF1_MOUSE
                                                                                                                                                                                                                                                  Qy
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RBMS_CHICK
                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                   OTFI_MOUSE STANDARD; PRT; 203 AA. 060753; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update)
   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                Mus musculus (Mouse)
                                                  CTF1.
                                                               Cardiotrophin-1 (CT-1).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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16-OCT 2001 (Rel. 40, Last sequence update)
16-OCT 2001 (Rel. 40, Last annotation update)
RNA-binding protein with multiple splicing homolog (RBP-MS) (HEart, RRM Expressed Sequence) (Hermes).
                                                                                                                                                                                                                                                                                                                                                                                       RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING HEART.
-!- DEVELOPMENTAL STAGE: MRNA ALREADY DETECTED AT STAGE 7-8 IN THE CARDIOGENIC MESODERM, AND BECOME ALMOST UNDETECTABLE IN THE OUTER CURVATURE OF THE VENTRICULAR REGION WHEREAS REMAINING HIGH IN THE DEVELOPING ATRIAL REGIONS.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the developing heart.";
Mech. Dev. 80:77-86(1999).
-!- FUNCTION: MAY BIND RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krieg P.A.;
"The RNA-binding protein gene, hermes, is expressed at high levels in
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF129933; AAD30273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerber W.V., Yatskievych T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99195799; PubMed=10096065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RBPMS OR HERMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9W611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RBMS_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                              Local Similarity hes 7; Conserv
                                                                                                                                                                                                                     171 AAAAAAL 177
                                                                                                                                                                                                                                                 8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00360; RRM;
                                                                                                                                                                                                                                                                                                                                             200 AA;
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                             169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                            100.0%;
   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                        21856 MW; 4093B3C780BBC1DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                              4.1%; Score 7; DB 1; 100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                     RNA-BINDING (RRM).
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antin P.B., Correia K.M., Conlon R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 AA
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                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                             Length 200;
                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                            0;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                    Q63507;

Ol-NOV-1997 (Rel. 35, Created)

Ol-NOV-1997 (Rel. 35, Last sequence update)

Ol-NOV-1997 (Rel. 35, Last annotation update)

60S_ribosomal protein L14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocyte hypertrophy.";
Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
-i- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BIN AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                         Chan Y.-L., Olvera J., Wool I.G.;
"The primary structure of rat ribosomal protein L14.";
Biochem. Biophys. Res. Commun. 222:427-431(1996).
-i- SIMILARITY: BELONGS TO THE L14E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pennica D., King K.L., Shaw K.J., Luis E., Rullamas J., Luoh
Darbonne W.C., Knutzon D.S., Yen R., Chien K.R., Baker J.B.,
                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-96222520; PubMed-8670222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL14_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U18366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
              EMBL; X94242; CAA63926.1;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-40 AND 119-141
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95166785; PubMed=7862649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR)/GP 130 RECEPTOR COMPLEX.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN
LIVER, LUNG AND KINNEY. LOWER LEVELS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXPRESSION IN SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:105115; Ctf1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AAALSVL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AAALSVL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an email to license@isb-sib.ch).
IPR000302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC52173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8B3D414A0B3B232F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 AA.
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                                                                                                  ormatics and the EMBL outstat:
There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                                                                                                      Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Luoh S.-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O. BINDS
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COBM_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                          Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Quairer S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRUU
Pfam; PF00467;
                                                                                                                                                                          STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Peterson J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg (
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg (
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Precorrin-4 C11-methyltransferase (EC 2.1.1.133) (Precorrin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COBM_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal protein; Repeat.
INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: METHYLTRANSFERASE THAT CATALYZES THE METHYLATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q10672;
15-JUL-1998
                                                                                                                                                                                                                                                                                Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COBM OR RV2071C OR MT2131 OR MTCY49.10C
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
                       AND CBIL/COBI.
                                      SIMILARITY: BELONGS TO A FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteria; Actinobacteria (class); Actinobacteridae;
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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173
178
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100.08;
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Pred. No
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                                       THAT GROUPS
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28;
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through a collaboration
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                                          CYSG,
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RESULT 16
GSHI_MOUSE
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                     SEQUENCE OF 146-205 FROM N.A.
MEDLINE=92073356; PubMed=1683707;
Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Potter S.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSHI_MOUSE STANDARD; PRT; 261 AA. P31315; 01-JUL-1993 (Rel. 26, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Homeobox protein GSH-1.
                                                                                                                                                                                                                                                                                                                                                                                                               development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96181350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NIH Swiss;
MEDLINE=96172995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev. Dyn. 203:337-351(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Gsh-1: a novel murine homeobox gene expressed in the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valerius M.T., Li H., Stock J.L., Weinstein M., Kaur S., Singh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000878; Cor/por_Metransf.
InterPro; IPR003043; Uropor_Metransf.
Pfam; PF005590; TP_methylase; 1.
PROSITE; PS00839; SUMT_1; 1.
PROSITE; PS00840; SUMT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE007063; AAK46411.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Zeitler P.S., Valerius M.T., Small K., Potter S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AAAAAAL 120
                                                                                                                                                                                                                                                                                                                                                                              15:714-724(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                  an orphan Hox gene, is required for normal pituitary
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100.0%;
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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o. 32;
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EMBL outstation
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A Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
A Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
A Natale D.A., Rogozin I.B., Tatusova R.L., Wolf Y.I., Stetter K.O.,
RA Malyhb A.G., Koonin E.V., Kozyavkin S.A.,
The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens."
RT Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -!- FUNCTION: Is responsible for channelling the electrons from the
CC oxidation of dihydroorotate from the FMN redox center in the pyrb
CC subunit to the ultimate electron acceptor NAD(+) (By similarity).
CC -!- CORACTOR: Binds a 2Fe-2S cluster and FAD (By similarity).
CC -!- SUBUNIT: Heterotetramer of 2 pyrK and 2 pyrD subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRK_METKA
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use by non-profit institute, There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                   similarity).
-!- SIMILARITY: BELONGS TO THE PYRK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-AV19 / DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRK OR MK0564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tb-UUN-2002 (Rel. 41, Last annotation update)
Probable dihydroorotate dehydrogenase electron transfer subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanopyrus kandleri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRK_METKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00046; homeobox; 1.
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SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A37290; A37290.
A38809; A38809.
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; 27727 мw;
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RESULT 18
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Best Local
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PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.

Pyrimidine biosynthesis; Transport; Electron transport; Metal-binding; Pyrimidine biosynthesis; Transport; Electron transport; Metal- Iron; Flavoproteain; FAD; Complete proteome SIMILARITY).

METAL 217 217 1RON-SULFUR 1 (2FE-2S) (BY SIMILARITY).

METAL 22 22 1RON-SULFUR 2 (2FE-2S) (BY SIMILARITY).

METAL 234 234 1RON-SULFUR 2 (2FE-2S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum "Complete genome sequence of Methanobacterium thermoautotrophicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tetrahydromethanopterin S-methyltransferase s
                                                                                                                                                                                                                                                                                                                                                                                                  deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

i. FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE FUNCTION: THE FORMATION OF METHYL-COENZYME M AND METHALYCONGENESIS, THE FORMATION OF METHYL-COENZYME M AND NS-METHYL-TETRAHYDROMETHANDPIERIN FROM COENZYME M AND NS-METHYL-COENZYME M AND NS-METHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTRC OR MTH1161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5-JUL-1999
                                                                                         modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Integral membrane protein.
                 Transferase; Methyltransferase; Transmembrane; Methanogenesis;
                                     TIGRFAMS; TIGR01148;
                                                         EMBL; AE000885; AAB85650.1;
                                                                                                                                                                                                                                                                                                                          TRANSLOCATING STEP (BY SIMILARITY).

CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
                                                                                                                                                                                                                                                                                        PATHWAY: Methanogenesis.
                                                                                                                                                                                                                                                                                                                                                                                  TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING, SODIUM-ION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE010350; AAM01779.1;
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                                                                                                                                                                                                                                                                                                            (methylthio)ethanesulfonate.
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 proteome
                                                                                                                                                       non-profit institutions as long
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262 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184A7D1CE99B6761 CRC64;
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                                                                                                                                                             as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 262;
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Best Local
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01-JUL-1993 (Rel. 26, Created)
01-JUN-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tetrahydromethanopterin S-methyltransferase subunit C (EC 2.1.1.86)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTRC_METIM
                                                                                                                                                                                                                                                               Eur.
                                                                                                                                                                                                                                                                                                                                                                                           N5-methyltetrahydromethanopterin: coenzyme-M methyltransferase from Methanobacterium thermoautotrophicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, sequencing and immunological characterization of the corrinoid-containing subunit of the
                                                                                                                                                                                                                                                                                                                                                                                                                                            Stupperich E., Juza A., Hoppert M., Mayer F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94039026; PubMed=8223548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=79929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunit C)
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-30.
MEDLINE=93238732; PubMed=8477726;
                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 217:115-121(1993).
            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum." Eur. J. Biochem. 213:537-545(1993).
                                                                                                                                                                                                                                                                                                     "Purification and properties of N5-methyltetrahydromethanopterin:openzyme M methyltransferase from
                                                                                                                                                                                                                                                                                                                              Gaertner P., Ecker A., Fischer R.
                                                                                                                                                                                                -
EMBL; X73123; CAA51554.1; -.
                                                              the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                           between
                                                                                                       This
                                                                                                                                                                                 TRANSLOCATING STEP.

CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2
                                                                                                                                                                                                                                    FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP METHANGENESIS, THE FORMATION OF METHYL-COENZYME M AND TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                         TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AAALSVL 146
                                                                                                                                                          PATHWAY:
                                                                                                                                                                       (methylthio)ethanesulfonate.
                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                               COMPOSED OF 8 DIFFERENT SUBUNITS.
                                                                                                                                                           Methanogenesis
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                                                                                                                                                                                                                                                                                                                                  Linder D., Fuchs G., Thauer R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266
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                                                                    There are no restrictions on ng as its content is in no
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Best Local
                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; AC009336; -; NOT_ANNOTATED_CDS.
EMBL; AY014304; AAG42152.1; -.
EMBL; AY014303; AAG42152.1; JOINED.
EMBL; X15507; CAA33529.1; -.
PIR; B32830; B32830.
PIR; S05957; S05957.
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                               "Complementary homeo protein gradients in developing limb Genes Dev. 3:641-650(1989).
                                                                                                                                                                                                                                                                       MEDLINE=89306602; PubMed=2568311;
Oliver G., Sidell N., Fiske N., Heinzmann C., Mohandas T.,
Sparkes R.S., de Robertis E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P13378;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homeobox protein Hox-D8 (Hox-4E) (Hox-5.4). HOXD8 OR HOX4E.
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                                                                                                                                                                                                                                                                                                                                                A complete mutation
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TIGRFAMS; TIGR01148;
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                                                                                                                                                                                  SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                               FUNCTION: SEQUENCE-SPÉCIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 AAALSVL 146
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                                                                                                                                                                                                                                                                                                                                  (NOV-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                           Suzuki T.,
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0; Mismatches
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Y -> S (IN REF.
                                                                                                                                                                                                                                                                                                                                           Panel of human HOX genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> S (IN REF. 2).
29843603282D7807 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                      PIR; S05508; S05508.
InterPro; IPR002628; PSII_MSP.
Pfam; PF01716; MSP; 1.
Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                                                                                               Mayfield S.P., Schirmer-Rahire G., Frank H., Zuber H., Rochaix J.-D. "Analysis of the genes of the OEE1 and OEE3 proteins of the photosystem II complex of Chlamydomonas reinhardtii."; Plant Mol. Biol. 12:683-693(198).

-i- FUNCTION: STABILIZES THE MANGANESE CLUSTER WHICH IS THE PRIMARY SITE OF WATER SPLITTING (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex.
                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
    Thylakoid; Membrane; TRANSIT 1
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                 EMBL; X13826; CAA32053.1; -.
                                                                                                                                                                                                                                                                                                                                              STRAIN=137c / CC-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxygen-evolving enhancer protein 1, chloroplast precursor (OEE1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00032; ANTENNAPEDIA; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P12853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSBO_CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00025; ANTENNAPEDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 142985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:5139; HOXD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T03332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 AA;
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109
197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMEOBOX_1; 1.
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50
123
256
287
  52 CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
CHLOROPLAST.
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G -> A (IN REF. 3).
; 75FF95A73E2AA85F CRC64;
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POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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o. 37;
                                                                                                                                                There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 290;
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                                                                                                                                                                                                                                                                                                                            Rochaix J.-D.;
                                                                                                                                                                                                                                              associated
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RESULT 23
GSH2_HUMAN
ID GSH2_HI
AC Q9BZM3;
DT 15-JUN-
DT 15-JUN-
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RBSK_BACHD
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                                                                                                                                     Matches
                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 28:4317-4331(2000).

- CARALYTIC ACTIVITY: ATP + D-ribose = ADP + D-ribose 5-phosphate.

- PATHWAY: Ribose metabolism; first step.

- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribokinase (EC 2.7.1.15).
RBSK OR BH3728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                      GSH2_HUMAN
Q9BZM3;
                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9K6K1;
                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus halodurans. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RBSK_BACHD
 15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                       PROSITE; PS00583; PFKB_KINASES_1; 1. PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                        InterPro; IPR002139; Pfam; PF00294; pfkB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                            Transferase; Kinase; Complete proteome
                                                                                                                                                                                                                             PRINTS; PR00990
                                                                                                                                                                                                                                                                         HSSP; P05054; 1RK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=86665;
                                                                                                                                                                                                                                                              InterPro; IPR002173; PfkB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                    Local Similarity
tes 7; Conserv
                                                                                          264
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                                                                                                                                                                                                                                                                                      AP001519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAL 14
                                                                                          AAAALSV 270
                                                                                                               AAAALSV 16
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291 AA;
                                                                                                                                                                                   294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
(Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                    STANDARD;
                                                                                                                                                                                                                                                                                     BAB07447.1; -.
                                                                                                                                                                                                                              RIBOKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
30522 MW;
                                                                                                                                                                                   31089 MW;
                                                                                                                                                 100.0%;
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                                                                                                                                                            4.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                     0;
                                                                                                                                                Score 7; DB 1; pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OXYGEN-EVOLVING ENHANCER PROTEIN 1.; 5DF4DFAEB1324267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                   8C13E0FCF5E89FDE CRC64;
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 AA.
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). 37;
                                    304 AA
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                                                                                                                                                           Length 294;
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                                                                                                                                         0;
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       GSH2_MOUSE
                                                                                                                                        RESULT 24
                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).

Homo sapiens (Human).

Metazoa; Chordata;
                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cools J., Marynen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last annotation update) Homeobox protein GSH-2.
                                                                                                                                                                                                                                                                                       Developmental protein.
DNA_BIND 202 261
DOMAIN 124 130
DOMAIN 134 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                GSH2 OR GSH-2
                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000047; HTH_repre
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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    NCBI_TaxID=10090;
                                                           Homeobox protein GSH-2.
                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox; 1.
                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                               AF306344;
AF306343;
P14653; 1B
                                                                                                                                                                           157 AAAAAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB028838;
                                                                                                                                                                                                                                                                                                                                                                   ; PD000010; Homec SM00389; HOX; 1.
                                                                                                                                                                                                8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                          PR00031; HTHREPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                   PR00024; HOMEOBOX
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                  147
304 AA;
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK00880.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAB84822.1; -. AAK00880.1; -.
                                                                                                                                                                                                                                                                                                                                                                                Homeobox; 1.
                                                                                                                                                                                                                                                                   162
32061 MW;
                                                                                                                                                                                                                                  4.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       HTH_repressr
                                                                                                                                                                                                                                 Score 7;
; Pred. No.
                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                               POLY-HIS.
                                                                                                                                                                                                                                                                                                      POLY-HIS.
                                                                                                                                                                                                                                                                                                                HOMEOBOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sakai T., Sakamoto S., Nakamura K., Muraki T.; "Human homeobox protein GSH-2."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Cincroaca; Catarrhini; Hominidae; Homo.
                                                                                                                                     GSH2_MOUSE STANDARD; PRT; 305 AA
p31316;
01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E896D5422488E6C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                        305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 304;
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RESULT 25
GVPL_HALME
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                                                                                                                                                                                                                                                                           Matches
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                                                                                              Q02237;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation updat
                                                     Halobacterium mediterranei (Haloferax mediterranei)
                                                                                     GvpL protein.
SEQUENCE FROM N.A
                       NCBI_TaxID=2252;
                                   Halobacteriaceae; Haloferax
                                             Archaea; Euryarchaeota;
                                                                                                                                                      GVPL_HALME
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B38809; B38809.
HSSP; P14653; 1B72.
MGD; MGI:95843; Gsh2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox. Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                        Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S79041; AAB34947.1; -. PIR; B37290; B37290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING BRAIN.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J., Copeland N.G., Potter S.S., "Identification of 10 murine homeobox genes."; Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92073356; PubMed=1683707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 203-262 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hsieh-Li H.M., Witte D.P., Szucsik J.C., Weinstein M., Li H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potter s.s.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95344993; PubMed=7619729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NIH Swiss;
                                                                                                                                                                                                                     158 AAAAAAL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 5'-CNAATTAG-3'
                                                                                                                                                                                                                                              8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. 50:177-186(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a murine homeobox gene expressed in the developing brain.";
                                                                                                                                                                                                                                                                                                                           147
305 AA;
                                                                                                                                                                                                                                                                                                                                                     124
134
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                              203
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                 4.1.,
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                        32167 MW;
                                                                                                                                                                                                                                                                                4.18; Score 7;
100.0%; Pred. N
                                          Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                              POLY-HIS.
                                                                                                                                                                                                                                                                                                                                     POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                          HOMEOBOX.
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                                                                                                                                                                                                                                                                                                                    51E7F2DB76E32608 CRC64;
                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                    322 AA.
                                                                                               update)
                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                           Length 305;
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                                                                                                                                                                                                                                                             0;
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
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Best Local
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MEDLINB-92275347; PubMed=1317319;
Grossniklaus U., Pearson R.K., Gehring W.J.;
"The Drosophila sloppy paired locus encodes two proteins involved in segmentation that show homology to mammalian transcription factors.";
Genes Dev. 6:1030-1051(1992).
                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P32030; Q9VQV4;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fork head domain transcription factor slp1 (Sloppy paired locus
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein 1).
SLP1 OR FD6 OR CG16738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             halophilic archaea.";
J. Mol. Biol. 227:586-592(1992).
-!- FUNCTION: MAY PLAY A STRUCTURAL OR REGULATORY ROLE IN GAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gas vesicle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X64701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Englert C., Krueger K., Offner S., Pfeifer F.;
"Three different but related gene clusters encoding gas vesicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=DSM 1411;
MEDLINE=93021102; PubMed=1404376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 QNRRAEL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 AA
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RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
C --- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN SEGMENTATION. REQUIRED
밁
                                                    δõ
                                                                                                                   Matches
                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X66095; CAA46889.1; -.
EMBL; X66096; CAA46890.1; -.
EMBL; AE003578; AAF51058.1; -.
PIR; $23053; $23053.
PIR; $23054; $23054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on the purpose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0003430; slp1.
InterPro; IPR001766; TF_Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                              proSITE; pS50039; FORK_HEAD_3; 1.
pna-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00657; FORK_HEAD_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000425; TF_Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00053; FORKHEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Pair-rule protein; Polymorphism.
DNA_BIND 119 210 FORK-HEAD.
                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                              VARIANT
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DEVELOPMENTAL STAGE: PRESENT AT 0-3 HRS OF EMBRYOGENESIS. MAXIMAL EXPRESSION AT 3-6 HRS. STRONG RE-EXPRESSION IN FIRST-INSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN SEGMENTATION. REQUIRED FOR THE FORMATION OF THE MANDIBULAR LOBE. DIFFERENT LEVELS OF SLP ACTIVITY SEEM TO BE REQUIRED IN DIFFERENT SEGMENTS.
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
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   257 AAAAAAL 263
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                                                        8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00658; FORK_HEAD_2;
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                                                                                                             36202 MW;
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p -> Q (IN STRAIN OREGON-R AND
'; 24CDE9F0102024C4 CRC64;
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                                                                                                                                                                                 DB 1;
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                                                                                                                               0;
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RESULT 27
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GDC AC DT DT DT DT DT DT
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                                                                                                                                           RESULT 28
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85
Antigen 85-B) (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun. 58:550-556(1990).

-i- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR THE HIGH AFFINITY OF WYCOBACTERIA TO FIBRONECTIN. POSSESSES A MYCOLYLITRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF TRENALOSE DINYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY FOR MAINTAINING CELL WALL INVESTIGATIVE (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Secreted.

-i- SUBCELLULAR TOCATION: SCOTTERIUM A85 ANTIGENS AND TO THE SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen of Mycobacterium kansasii.";
Infect. Immun. 58:550-556(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsuo K., Yamaguchi R., Yamazaki A., Tasaka H., Terasaka K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=90129315; PubMed=2404875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium kansasii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fibronectin-binding protein B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Acyltransferase; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X53897; CAA37868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                 GDC_BOVIN STANDARD; PRT; 330 AA (201888; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00756; Esterase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P31953; 1DQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A37185; A37185.
               Grave's disease carrier protein (GDC) (Mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
protein homolog).
                                                                                                                                                                                                                                                                    Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-TERMINAL OF C.GLUTAMICUM PS1 PROTEIN.
                                                                                                                                                                                                19 AAAAAAL 25
                                                                                                                                                                                                                                    8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and expression of the gene for the cross-reactive alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000801; Esterase_put.
                                                                                                                                                                                                                                                                                                                                           325 AA;
                                                                                                                                                                                                                                                                  ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                            325
166
270
302
                                                                                                                                                                                                                                                                                                                                               34323 MW;
                                                                                                                                                                                                                                                                         4.1%; Score 7; DB 1;
100.0%; Pred. No. 40;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                ANTIGEN 85-B.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                               5F2281BCC48AE30D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 AA
                                                                                                                  330 AA
                                         update)
                                                                                                                                                                                                                                                                                                               Length 325;
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                   0;
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RESULT 29
RLAO_METGA
ID RLAO
AC P5404
AC P5407
AC P5407
DT 15-0C
DT 16-0C
DE Acidi
GN RPLPO
OS Metha
OC Archa
OC Metha
OC NCBL
RN [1]
RN [1]
RN SEQUE
RC STRAIL
RX MEDLI
                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
MEDLINE=96337999; PubMed=8688087;
                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                   Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                     Methanococcus jannaschii
                                                                                                                        RPLPO OR MJ0509
                                                                                                                             Acidic ribosomal protein PO homolog (LIOE),
                               SEQUENCE FROM N.A
                                                           NCBI_TaxID=2190;
                                                                                                                                                                                                           RLAO_METJA
                                                                                                                                                                                                                           METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; $26596, $26596.

Interpro; IPR002067; Mit_carrier.

Interpro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X66035; CAA46834.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence and pattern of expression of a bovine homologue of a human mitochondrial transport protein associated with Grave's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Required for the accumulation of coenzyme A in the mitochondrial matrix (By similarity).
-i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93091248; PubMed=1457817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLC25A16 OR GDA OR GDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane (By similarity).
TISSUE SPECIFICITY: MOSTLY IN THYROID, LIVER, LUNG, KIDNEY AND
TO A LESSER EXTENT IN HEART AND SKELETAL MUSCLE.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                              8 AAAAAAL 14
                                                                                                                                                                                                                                                                                  2 AAAAAAL 8
                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    218
330 AA;
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              132
189
232
               / DSM 2661 / ATCC 43067
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                      100.0%; Preu. ...
+ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               152
209
252
121
                                                                                                                                                                                                                                                                                                                                                                                                 36085 MW;
                                                                                                                                                                                                                                                                                                                                                       4.1%; Score 7;
100.0%; Pred. N
                                                                                                                                                                                                                                                                                                                                                                                                                 ω
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                              4C614701D2B8DEA9 CRC64;
                                                                                                                                                                                                       338 AA
                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                Length 330;
                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                 0;
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GUB_FIBSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                             beta-glucanase (1,3-1,4-beta-D-glucan 4-glucanohydrolase) gene.";
J. Bacteriol. 172:3837-3841(1990).
-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
                                                                                                                                           in beta-D-glucans containing 1,3- and 1,4-bonds.
-!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                           MEDLINE=90299807; PubMed=2193918;
Teather R.M., Erfle J.D.;
"DNA sequence of a Fibrobacter succinogenes mixed-linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Beta-glucanase precursor (EC 3.2.I.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Mixed linkage beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUB_FIBSU
P17989;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 28-57 STRAIN-ISOlate S85;
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Fibrobacter/Acidobacteria group; Fibrobacter group
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibrobacter succinogenes (Bacteroides succinogenes)
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein; Complete proteome. SEQUENCE 338 AA; 36751 MW; 63A6AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weinstock K.G., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M., Klenk H.-P., Frasser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00466; Ribosomal_L10; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001790; Ribosomal_L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: RIBOSOMÁL PRÓTEIN PO IS THE FUNCTIONAL EQUIVALENT OF E.COLI PROTEIN L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rigr; mJ0509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 ALASKLP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ALASKLP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U67500; AAB98499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 7; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT
DKK3_H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M33676; AAA24896.1;
PIR; A44507; A44507.
HSSP; P23904; LAJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UBE4; Q9ULB7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [nterPro; IPR000757; Glyco_hydro_16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (hDkk-3).
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DKK3 OR REIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKK3_HUMAN
                                                                                                                                                                                                                                                                                        Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W., Amarzavadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B., Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A., "Functional and structural diversity of the human Dickkopf gene
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                            Tsuji T., Miyazaki M., Sakaguchi M., Inoue Y., Namba M.; "A REIC gene shows down-regulation in human immortalized cells and human tumor-derived cell lines.";
                                                                                                                                                                    MEDLINE=20119095; PubMed=10652205;
Tsuji T., Miyazaki M., Sakaduchi M
                                                                                                                                                                                                                 Tanaka S., Sugimachi K.,
Submitted (OCT-1999) to
                                                                                                                                                                                                                                                                    Gene
                                                                                                                                                                                                                                                                                                                                        MEDLINE=20035735; PubMed=10570958;
                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
Kobayashi K., Ouchida M., Tsuji T., Hanafusa H., Miyazaki M., Namba M., Shimizu N., Shimizu K.; "Reduced expression of the REIC/Dkk-3 gene by promoter-hypermethylation in human tumor cells.";
                                                                                              Tate G.,
                                                                                                                               Biochem. Biophys. Res. Commun. 268:20-24(2000)
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               family
                                                                                   Submitted (NOV-1999)
                                                pubMed=11814687;
                                                             SEQUENCE FROM N.A.
                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                    238:301-313(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00722; Glyco_hydro_1
PS01034; GLYCOSYL H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAAL 14
                                                                                                 Mitsuya T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOSYL_HYDROL_F16; 1.
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79
83
307
277
284
291
298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%;
                                                                                     to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Repeat.
                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                  Sugimachi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY)
5 X 7 AA TANDEM REPEATS OF P
                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16DC4F5BDEFC578A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA TANDEM REPEATS OF P-X-S-S-S-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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SOTETE TET WERE READED FOR THE STATE OF THE 
QY
                                                                                                                                                                                                                                                                                                      RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 605416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Developmental protein;
                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                     KLF2 OR LKLF.
Mus musculus (Mouse)
                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kruppel-like factor 2 (Lung kruppel-like factor).
                                                                                                                                                                                                                                        Q60843;
                                                                                                                                                                                                                                                            KLF2_MOUSE
  SEQUENCE FROM N.A
                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: N-GLYCOSYLATED.
SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB035205; BAA87044.2; JOINI
AB045206; BAA87044.2; JOINI
AB045205; BAA87044.2; JOINI
AB045205; BAA87044.2; JOINI
AB045206; BAA87044.2; JOINI
AB045206; BAA87044.2; JOINI
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AB045208; BAA87044.2; JOINI
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AB045208; BAA87044.2; JOINI
AB045209; BAA87044.2; JOINI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC007660; AAH07660.1;
                                                                                                                                                                                                                                                                                                                                                                         338 AAAAAAL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB057804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB057591; BAB84360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB045210; BAA87044.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:2893; DKK3.
                                                                                                                                                                                                                                                                                                                                                                                                                  8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                 STANDARD;
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195
284
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306
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121
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JOINED.
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . . .)
G-S R (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7; DB 1; ; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKK-TYPE CYS-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
DICKKOPF RELATED PROTEIN-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKK-TYPE CYS-
                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein.
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72F504122B40AFFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                        354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .) (POTENTIAL)
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) (POTENTIAL).
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whi outstation -
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KLF2_HU
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                      KLF2_HUMAN STANDARD; PRT; 355 AA. 09Y5W3; 09UKR6; 09UJS5; 30-MAY-2000 (Rel. 39, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Kruppel-like factor 2 (Lung kruppel-like factor).
Kozyrev S.V., Hansen L.L., Poltaraus A.B., Domninsky D.A.,
                                                                                HOMO Sapiens (Human).
Homo sapiens (Human).
Finkarvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                   HUMAN
                                                   SEQUENCE FROM N.A.
                                                                                                                                     KLF2 OR LKLF
                      MEDLINE=99231781; PubMed=10217429;
                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00028; zINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; zINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00048; ZINCFINGER, ProDom; PD000003; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is so long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1342772; Klf2.
InterPro; IPR000822; Zn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T01677; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U25096; AAA86728.1; -. HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multigene family.";
Mol. Cell. Biol. 15:5957-5965(1995).
-i- FUNCTION: BINDS TO THE CACCC BOX IN THE BETA-GLOBIN GENE PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Anderson K.P., Kern C.B., Crable S.C., Lingrel J.B.,
"Isolation of a gene encoding a functional zinc finger protein
homologous to erythroid Kruppel-like factor: identification of a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6 X CBA; TISSUE=Lung; MEDLINE=96025976; PubMed=7565748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPIEEN.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND ACTIVATES TRANSCRIPTION. Similarity). SUBCELLULAR LOCATION: Nuclear (By similarity). TISSUE SPECIFICITY: PREDOMINANT EXPRESSION IN THE LUNGS AND
                                                                                                                                                                                                                                                                                     225 AAAAAAL 231
                                                                                                                                                                                                                                                                                                                 8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                              354 AA;
                                                                                                                                                                                                                                                                                                                                                  4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             37700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r protein; Repeat
70 POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC FINGERS
                                                                                                                                                                                                                                                                                                                                                                                    C4A99D018AC5BAF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                             Length 354;
                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                         Matches
                                                                                                                                                     Query Match
                                                                                                                                                                                                                                 CONFLICT
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Probom; PD000003; Znf_C2H2; 2.
SMART; SM00355; Znf_C2H2; 3.
SMART; SM00355; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Lee H.J., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J.,

Lee H.J., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J.,

Sohn M.Y., Hwang S.Y., Im S.U., Jung E.J., Kim J.C.,

"A catalogue of genes in the human dermal papilla cells as identified

by expressed sequence tags.",

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: BINDS TO THE CACCC BOX IN THE BETA-GLOBIN GENE PROMOTER

AND ACTIVATES TRANSCRIPTION (BY SIMILARITY).

-i- SUBGELIULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SUBGELIULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulat
                                                                                                                                                                                                                                                                                                                                   N_FING
                                                                                                                                                                                                                                                                                                                                                           ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T04958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99389728; PubMed=10458913; Wani M.A., Conkright M.D., Jeffries S., Hughes M.J., Lingrel J.B.; "CDNA isolation, genomic structure, regulation, and chromosomal localization of human lung kruppel-like factor."; Genomics 60:78-86(1999).
                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 448:149-152(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of the human CpG-island-containing lung Kruppel-like factor (LKLF) gene and its location in chromosome 19p13.11-13 locus.";
226 AAAAAAL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602016; -
                                              8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF123344; AAD25076.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF205849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:6347; KLF2.
                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                              355 AA;
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1SP2.
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AAF13295.1;
                                                                                                                                                                                                37419 MW;
                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                               4.18;
                                                                                               0;
                                                                                                                  Score 7; Pred. No.
                                                                                                                                                                                                                 C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
S > N (IN REF.
L >> P (IN REF.
P -> S (IN REF.
P -> M (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY.
                                                                                                                                                                                      D5849C831D676AE1 CRC64;
                                                                                            Mismatches
                                                                                                                  DB 1;
o. 44;
                                                                                      0;
                                                                                                                                     Length 355;
                                                                                 0;
                                                                              Gaps
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BET3_MESAU

BET3_MESAU

STANDARD;

367 AA

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                                                                                                                                                                                               RESULT
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30-мау-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96140430; PubMed=8552091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsai M.-J.;
"BETA3, a novel helix-loop-helix protein, can act as a negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulator of BETA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S80870; AAB50691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00353; HLH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00010; HLH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFAC; T01674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001092; HLH_basic.
                                                 01-NOY-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
Hypothetical protein ycbU precursor. YCBU.
                                                                                                                                                                            BACSU
                                                                                                                        P42253;
                                                                                                                                                CBU_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liator of BETA2 and MyOD responsive genes.";

Cell. Biol. 16:526-633(1996).

Cell. Biol. 16:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: KIDNEY, LUNG, BRAIN AND PANCREAS (INSULINOMA). SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCULULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH CLASS A BASIC HELIX-LOOP-HELIX FACTORS. DESPITE THE PRESENCE OF AN INTACT BASIC DOMAIN, DOES NOT BIND TO DNA.
                                                                                                                                                                                                                                                                           314 AAAAAAL 320
                                                                                                                                                                                                                                                                                                                          8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                           034388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 39, Rel. 39, Rel. 39, Rel. 40, Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLH_1; 1.
HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35905 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; I
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; Repressor
                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 367;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RA Kurita K., Lapidus A., Lardinolis S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
RA Lee S.M., Levine A. Liu H., Masuda S., Mauel C., Medique C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M.,
RA Persecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Takagi T., Takahashi H., Takamaru K.,
RA Sorokin A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takauchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takauchi M., Vanienbol M., Vanier F., Vassarotti A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vanier F., Vassarotti A.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Vanier S., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Ehrlich S.D., Emmerson P.T., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Kumano M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Joris B., Klaerr-Blanchard M., Klein C., Joris B., Klaerr-Blanchard M., Klein C., Joris B., Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A 32 kb nucleotide sequence from the region of the lincomycin-
resistance gene (22-25 degree) of the Bacillus subtilis chromosome and
identification of the site of the lin-2 mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.; "Determination of a 21548 bp nucleotide sequence around the degrees region of the Bacillus subtilis chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95219079; PubMed=7704254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-319 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its tase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 141:269-275(1995).
                                                                                                                                                                                                                                                                                                                                                                              peptidase of Bacillus subtilis."; FEBS_Lett. 305:67-73(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-147 FROM N.A.
                                                                                                                                                                                                                                                                             -!- CAUTION: Ref.3 sequence differs from that shown due to two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Awade A., Cleuziat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92339527; PubMed=1353026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  wade A., Cleuziat P., Gonzales T., Robert-Baudouy J.; {}^{\circ} "Characterization of the pop gene encoding the pyrrolidone carboxyl
                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                    frameshifts.
                                                                                                                                                                                                                                                                                                                        AMINOTRANSFERASES.
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FL_ORYSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                          Nuclear protein; Developmental protein.
DOMAIN 22 37 POLY-PRO.
                                             Pfam; PF01698; FLO_LFY; 1.
Transcription regulation; Activator; DNA-binding;
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                Kyozuka I, Konishi S., Nemoto K., Izawa T., Shimamoto K.,
"Down-regulation of RFL, the FLO/LFY homolog of rice, accompanied
"Down-regulation of RFL, the FLO/LFY homolog of rice, accompanied
"Doc. Natl. Acad. Sci. U.S.A. 95:1979-1982(1998).
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: In very young panicle but not in mature
florets, mature leaves, roots or apical meristems.
-!- SIMILARITY: BELONGS TO THE FLO / LFY FAMILY.
                                                                               EMBL; AB005620; BAA21547.1; InterPro; IPR002910; FLO_LFY.
                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Cryzae; Oryzae; Oryzae; Oryzae; Oryzae; Oryzae;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98151445; PubMed=9482818;
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024175;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative transcription factor FL (RFL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB000617; BAA22277.1; EMBL; 299105; CAB12060.1; EMBL; D30808; NOT_ANNOTATED_CDS.EMBL; X66034; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyridoxal phosphate; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Signal; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SubtiList; BG11176; ycbU.
InterPro; IPR000192; AminotransfV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 AAAAALS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                               Toride; TISSUE=Panicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
92
133
319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aminotran_5;
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370
207
92
133
319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1%; Score 7; DB 1
100.0%; Pred. No. 45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40809 MW;
POLY-PRO.
POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Best Local (
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                                                                                                                              Homeobox; DNA-binding; Nuclear protein; Transcription regulation DOMAIN 39 48 POLY-GLY.
                                                                                                                                                                                              PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox
                                                                                                                                                                                                                                                  TRANSFAC; T03420; -...
Genew; HGNC:4979; HLXB9.
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                                                                                                                                                                                                                                                                                                                                                                                                            Harrison K.A., Druey K.M., Deguchi Y., Tuscano J.M., Kehrl J.H.;
"A novel human homeobox gene distantly related to proboscipedia is expressed in lymphoid and pancreatic tissues.";
J. Biol. Chem. 269:19968-19975/1994)
-1- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR.
-1- SUBCELLULAR LOCATION: Nuclear
-1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND PANCREATIC TISSUES.
                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                  InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                               MIM; 142994;
                                                                                                                                                                                                                                                                                                 EMBL; U07664; AAB60647.1;
                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            EMBL; U07663; AAB60647.1; HSSP; P14653; 1B72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94327547; PubMed=7914194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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8 AAAAAAL 14
                          Similarity 7; Conserv
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                                                                      401 AA;
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                               100.0%;
                                                                 40932 MW;
             4.1%; Score 7; DB 1; 100.0%; Pred. No. 48; ive 0; Mismatches
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                                                            0006AEAD71D594FE CRC64;
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01-MOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
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MEDLINE-92201635; PubMed-1551572;
Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.;
"The mitochondrial genomes of two nematodes, Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWEL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute as long as its content is in no way use by non-profit institutions as long as its content is in no way
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Genetics 130:471-498(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                             p36578; p39029; Q969Z9;
01-JUN-1994 (Rel. 29, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
60s ribosomal protein L4 (L1).
MEDLINE-94092742; PubMed-8268230;
Bagni C., Mariottini P., Annesi F., Amaldi F.;
Bagni C., Mariottini P., Annesi F., Amaldi F.;
"Human ribosomal protein L4: cloning and sequencing of the cDNA and primary structure of the protein.";
primary structure of the protein.";
Biochim. Biophys. Acta 1216:475-478(1993).
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                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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rPro; IPR001750; Oxidored_q1.
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AA; 47064 MW; A4B135C1CA5587B6 CRC64;
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REVISIONS.
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Genome Res. 12:379-390(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshihama M., Uechi T., Asakawa S., Kawasaki K., Kato S., Higa S., Waeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lymphoma;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00939; RIBOSOMAL_L1E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
TUD4_AGRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BL; BC001365; AAH01365.1; --
BL; BC0051365; AAH01365.1; --
BL; BC007259; AAH07259.1; --
3L; BC007259; AAH07259.1; --
3L; BC007748; AAH07746.1; --
4, BC009888; AAH07996.1; --
4, BC010151; AAH10151.1; --
4, BC010151; BC010151; BC010151; --
4, BC010151; BC010151; BC010151; --
4, BC010151; BC01015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO THE L4E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S37197; S37197,
S39803; S39803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X73974; CAA52154.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L20868; AAA60281.1; ALT_SEQ. D23660; BAA04887.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC014653; AAH14653.1;
AB061820; BAB79458.1;
                                                                                                                                                                     355 AAAAAAL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:10353; RPL4.
                                                                                                                                                                                                                               8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002136; Ribosomal_L4/L1E
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363
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AAH14653.1; -.
BAB79458.1; -.
                    STANDARD;
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63
147
201
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                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> M (IN REF. 1).
S -> R (IN REF. 1).
V -> F (IN REF. 1).
MISSING (IN REF. 1).
                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C -> V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYS-RICH
                                                                                                                                                                                                                                                                                                                                                 Pred.
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5. 51;
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Search completed: July 6, 2003, 14:20:46 Job time: 20 secs
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Best Local Similarity 100.0%; p
Matches 7; Conservative 0;
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                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entitied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         Crouzet P., Otten L.;

"Sequence and mutational analysis of a tartrate utilization operon from Agrobacterium vitis.";

J. Bacteriol. 177:6518-6526(1995).

-i- FUNCTION: DEGRADES AN UNIDENTIFIED TOXIC PRODUCT FROM THE FIRST STEP OF TARTRATE DEGRADATION.

-i- CATALYTIC ACTIVITY: D-glycerate + NAD(P)(+) = hydroxypyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Tartrate degradation; second step.
                                                                                                                                                                                                                                                                                                                                                                                              -!- INDUCTION: BY TARTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium. NCBI_TaxID-373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q44472;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative hydroxypyruvate reductase (EC 1.1.1.81).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96062236; PubMed=7592429;
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                                                                 276 AAAAAAL 282
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                                                                                                                              4.1%; Score 7; DB 1; Length 438; 100.0%; Pred. No. 52;
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172
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          GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                         Q9x0g9 thermotoga Q8sIr2 oryza sativ Q9bij7 drosophila Q93np5 escherichia Q930c4 rhizobium m Q9vv18 drosophila Q996ct0 rhizobium 1
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Q94ea6 oryza sativ
Q9vqm0 drosophila
Q46112 drosophila
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Q51489 pseudomonas
Q91424 pseudomonas
Q91424 pseudomonas
Q98f85 rhizobium 1
Q44662 brucella ab
Q89mx7 anabaena sp
Q9vpl1 drosophila
Q8y144 ralstonia s
Q92f9 mus musculu
Q91w12 oryza sativ
Q8xfh6 salmonella
Q9yba7 aeropyrum p
Q9smy4 arabidopsis
Q926G3 rhizobium m
Q8u915 agrobacteri
Q9rtg4 deinococcus
Q9nmr9 leishmania
Q919s1 white spot
Q9pez5 xylella fas
Q91783 chlamydophi
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0960rl drosophila
09bmz8 drosophila
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0962d2 drosophila
09c2d1 drosophila
09c6d1 drosophila
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Q9ct43 mus musculu
Q9dgr5 oryza sativ
Q9kzf6 streptomyce
Q07218 mycobacteri
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Q91111 white spot
O9bmp6 culicoides
O9yh51 pseudopleur
O99013 pseudopleur
O94300 oryza sativ
O94300 oryza sativ
O94291 oryza sativ
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O94639 oryza sativ
O991v4 human immun
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Q9frv2 oryza sativ
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Q8x1x2 aspergillus
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Q957v5 arabidopsis
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Q9w0e6 drosophila
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Q9sa42 arabidopsis
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Q9PC85
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                                                        Query Match
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                 InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
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                                    Conservative
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                                                                                                                                   20431 MW; C8DD2F6233DB0C92 CRC64;
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Q9z7c5 chlamydia p
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Bayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtls K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Charley J.M., Cawley S., Dahlke C., Davenport L., D., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L., D., Dietz S.M., RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Sasaki T., Matsumoto T.,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McIecod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Munt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q. Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
DR RIBL; AE00358; AAF51145.;
DR RIBL; AE00369; THOL_PROTEASE_HIS; UNKNOWN_1.
Science 287.2165 aA; 234786 MW; F26344DB2EICAFD4 CRC64;
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"The Drosophila toucan (too) gene is required in germline cells the somatic cell patterning during coogenesis.";
Development 124:4917-4926(1997).
EMBL; Y14157; CAA74574.1;
FlyBase; FBgn001560; toc.
InterPro; IPR000169; SHProtLacsite.
PROSITE; P800639; THTOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 2176 AA; 235405 MW; 35ABBDE00B49EFC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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01-JUN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                       8 AAAAAALSV 16
                                                                                                                     Similarity 9; Conserv
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100.0%; Pred. No
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative UDP-glucuronic acid decarboxylase.
p0506B12.31.
                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                  "Oryza_sativa_nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=39947;
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Pfam; PF02502; LacAB_rpiB; 1.
TIGRPAMS; TIGR00689; rpiB_lacA_lacB; 1.
Isomerase; Complete proteome.
Isomerase; Complete proteome.
SEQUENCE 143 AA; 15867 MW; 3E17D72A10FFCCBD CRC64;
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Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.";

EMBL: AE001768; AAD38157.1;

Thierpro. IED007500. Eis. C. 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLEL. 21, Last annotation update)
                                                   Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003500; Rib/Gal_isomrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga maritima.
Bacteria; Thermotogae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 8; Conserv
                                                                                                                                                            AP003271; BAB89759.1; -.
NCE 249 AA; 26592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NYLLGKGI 137
64 SKLPSLVY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 NYLLGKGI 27
                                                                                                                                                                                                                                                                                                         T., Matsumoto T.,
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                           4.7%; Score 8;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.7%; Score 8;
100.0%; Pred. N
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                                                                                                                                                                                                                                                                                                         Yamamoto K.;
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                      7954F613B241E81F CRC64;
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                                                Mismatches
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                                                                                                DB 10; Length 249;
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o. 7.5;
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                                       Gaps
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SKLPSLVY 32

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ACCOMPANDACTOR OF THE PROPERTY OF THE PROPERTY
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                                                                                                              Matches
                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DNA-binding transcriptional repressor giant (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas J., Arnosti D.N.; submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF356543; AAK28631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09віл7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q93NP5
Q93NP5;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ВΙJ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0044278; Dhyd\gt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WBWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wbwc
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                                                                                                                                                                                                                         EMBL; AF361371; AAK64375.1; ...
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1
SEQUENCE 268 AA; 31176 MW; ClEF300
                                                                                                                                                                                                                                                                                                                         of 0104 specific genes.";
Gene 270:231-236(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Reeves P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21297197; PubMed=11404020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence of the E. coli 0104 antigen gene cluster and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
239 TGVIYTGV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 AAAAAALS 38
                                                       42 TGVIYTGV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conserv
                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Briggs C.E., Rothemund D., Fratamico P., Luchansky J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26948 MW; 09C0CA545CE455EA CRC64;
                                                                                                     4./,
100.0%; Pt
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                  Score 8; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                              Pred.
                                                                                                                                                                                                                               C1EF30C136A668F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                 Mismatches
                                                                                                                                              No.
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                                                                                                                                                                        Length 268;
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RESULT 9

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,
RA Grand R.C., Bould S., Hell G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Davendle J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Botkhakov S.,
RA Burtis K.C., Basm D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA George R.A., Doup J.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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Barloy Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
"Nucleotide sequence and predicted functions of the entire
sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL. AB007220; AAK64932.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RA0274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q930C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA0274 OR SMA0520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid; Hypothetical protein; Complete proteome. SEQUENCE 280 AA; 30615 MW; FF533F65700FC352 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VVI8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09VVI8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG6273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AAAAAALS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08; F1
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19,
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RESULT 11
Q986T0
ID Q986T0
AC Q986T1
D Q986T1
DT Q1-QC2
DT Q1-QC2
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Best Local :
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desorhizobium loti.,
DNA Res. 7:331-338(2000).
DNA Res. 7:331-338(2000).
DNA Res. 7:331-338(2000).
DNA Res. 7:331-38(2000).
DNA Res. 7:331-38(2000).
DNA Res. 7:331-38(2000).
InterPro; IPR002173; PfkB.
InterPro; IPR002174; PfkB.
InterPro; IPR002173; IPR002174; IPR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S. Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Complete genome structure of the nitrogen-fixing symbiotic bacterium
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last seq.
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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269 AAAAAALS 276
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100.0%; Pred. No.
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Last annotation update
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o. 15;
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Q9NGI8
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Q9NGI9
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                                                                                                                             Begun D.J., Whitley P.; "Reduced X-linked nucleotide polymorphism in Drosophila simulans."; Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
EMBL; AF252667; AAF68049.1.; -.
                                                                                               SEQUENCE
                                                                                                            NON_TER
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                                                                                                                                                                                                                                                 Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                      Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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EMBL; AF252666; AAF58048.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musce
Ephydroidea; Drosophilidae; Drosophila.
                                                           Local
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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269 AAAAAALS 276
                      8 AAAAAALS 15
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                                           Similarity 100.0%; 18; Conservative 0;
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                                                                                    32373 MW; 5ECC6A8C4546A230 CRC64;
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                                                     4.7%; Score 8;
100.0%; Pred. No.
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                                                                 DB 5;
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                                         0;
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RESULT 14
Q9NGI7
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ID Q9NGB
AC Q9NGB
AC Q9NGB
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DT 01-JU
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OC Ptery
OC Ptery
OC Ptery
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RRP SEQUI
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RT "Redd
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Pterygota; Neoptera; Endopterygota; Diptera;
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EMBL; AF252668; AAF68050.1; -.
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Q9NGB4;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                     NON_TER
                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20283933; PubMed=10823947;

Megun D.J., Whitley P.;

Reduced X. linked nucleotide polymorphism in Drosophila simulans.";

Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).

EMBL; AF255314; AAF68611.1;

EMBL; AF255314; AAF68611.1;
                                                                                                                                                                                                                                                                                                             Drosophila yakuba (Fruit fly).
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                                                                                                                                               FlyBase; FBgn0041640; Dyak\osa.
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                                                                                                          SEQUENCE
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 269
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                                                    l Similarity
8; Conserv
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100.0%; Pred. No.
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RESULT 16

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7240;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Begun D.J., Whitley P.;
"Reduced X-linked nucleotide polymorphism in Drosophila simulans.";
Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
EMBL; AF252670; AAF68052.1; ...
EMBL; AF252665; AAF68047.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eyelid (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20283933; PubMed=10823947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SIM7
                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0041660; Dsim\osa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                     Q9N6K2;
                                                                                                                                                                                                                                                                                                                                                                                                 Q9N6K2
                                                                                                                                                                                                                                                                                                                                      Eyelid (Fragment).
                                                                                                            NON_TER
                                                                                                                                                                        Begun D.J., Whitley P.; "Reduced X-linked nucleotide polymorphism in Drosophila simulans."; proc. Natl. Acad. Sci. U.S.A. 97:5980-5965(2000).
                                                                                                                                                                                                            STRAIN-SIM8, AND SIM6;
MEDLINE-20283933; PubMed-10823947;
                                                                                                                                                  EMBL;
                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                  FlyBase; FBgn0041660; Dsim\osa.
                                                                                                SEQUENCE
                                                                                                                                                                                                                                                             WCBI_TaxID=7240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AAAAAALS 276
                                                                                                                                                  Natl. Acad. Sci. 0.5.6.
AF252671; AAF68053.1; ...
AF252669; AAF68051.1; ...
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269 AAAAAALS 276
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                         8 AAAAAALS 15
                                                             Similarity
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                                                                                                    324 AA;
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                                                  Conservative
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100.0%; Pred. No.
                                                                 100.0%;
                                                                                                  32407 MW; 44676F22EA5071F0 CRC64;
                                                                            4.7%; Score 8;
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                                                                Pred.
                                                    Pred. No. 15;
Mismatches
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Q8X1X2
 Query Match
Best Local Similarity
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OBX1Z2; 12.002 (TIEMBLICAL 20, C
01-MAR-2002 (TIEMBLICAL 20, I
01-JUN-2002 (TIEMBLICAL 21, I
                                                                                                                                                                                   Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G.; Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K. T., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Whitehead S., Spratt B.G., Barrell B.G.; Tomplete DNA sequence of a serogroup A strain of Neisseria
                                                                 Pfam; PF01225; Mur_ligase; ī. Pfam; PF02875; Mur_ligase_C; 1. TIGRFAMS; TIGR01143; murF; 1.
                                                                                                       HSSP; P11880; 1GG4.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                                                                          Q9JSZ1;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
QDP-MurNAC-pentapeptide synthetase (EC 6.3.2.15).
                                                                                                                                                                                                                                                                                        STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                  meningitidis Z2491."
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Two pectin lyase genes (pelA and pelB) from Aspergillus oryzae KBN616: their sequence analyses and overexpression, and characterization of the gene products."; submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB029322; BAB82467.1; InterPro; IPR002022; Amb_allergen.
                                                                                                                                                                Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=65699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitamoto N.;
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                                                                                                                                                  AL162758; CAB85286.1; -.
                                        Complete proteome.
E 452 AA; 48112 MW;
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100.0%; Pred. N
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 100.0%;
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Score 8; 1; Pred. No.
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Last sequ
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Last annotation update)
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                                        9903D4DD1B64C4A9 CRC64;
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          DB 16; Length 452;
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Q981K5
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Best Local
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SEQUENCE FROM N.A.

STRAIN=ATCC 15992 / PAO1;

MEDLINE=20437337; pubMed=10984043;

Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Safer R.L., Collter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP002999; BAB49511.1; -.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
ProDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Complete pr
SEQUENCE 504 AA; 53754 MW; AE
                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                                                                                                                                                                                                        PA5317
                                                                                                                                                                                                                                                   Probable binding
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                                                                                                                                                                               NCBI_TaxID=287;
                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                             Q9HTN7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamot Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein mlr2359
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01-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha
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                                                                                                                                                                                                                                                                                                                                                                                                282
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(TrembLrel. 18, Last seq.
(TrembLrel. 20, Last ann
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100.0%; Pred. N
                                                                                                                                                                                                                                              component of ABC dipeptide transporter
                                                                                                                                                                                                    gamma subdivision; Pseudomonadaceae;
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A8DC1D5759D0D0FB CRC64;
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01-MAY-2000
01-MAY-2000
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01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T16011.4 protein (AT3G09000/T16011_4).
T16011.4 OR MZB10.3.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:959-964(2000).
EMBL; AE004944; AAG08702.1; -..
HSSP; P23847; 1DPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 1.
                                                                                                                                                                                                                                             Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kamiya A., Karlin-Neumann G., Kamiya A., Karlin-Neumann G., Narusaka Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Ronning.C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC T16011 genomic sequence."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III P1 MZB10 genomic sequence.";
                                                                                                                                                              "Arabidopsis cDNA clones.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AC010871; AAF07827.1; -.
EMBL; AC0109326; AAD56316.1; -.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  Ecker J.R.
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                                                                                                                                                AF428276; AAL16108.1; -.
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                                                                                                                                  541 AA;
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EMBL, AY061006; ARL28554 1; T.

ElyBase; FBgn0028577; pUbsf.

InterPro; IPR000504; RNA_rec_mot.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; 15.7.

Pfam; PF00076; rrm; 3.

PROSITE; PS50102; RRM; 3.

PROSITE; PS00030; RRM_RNP_1; UNKNOWN_2.

PROSITE; PS00030; RRM_RNP_1; E75E378!
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01-DEC-2001
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                                                                                                "A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading bacterium Pseudomonas abietaniphila BKME-9.";
J. Bacteriol. 181:2675-2682(1999).
EMBL; AF119621; AAD21067.1;
                                                                                                                                                                                                                                                                                                                                       Syst. Appl. Microbiol. 0:0-0(1999).
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                                                                                                                                                                                                                              MEDLINE=99235742; PubMed=10217753;
                                                                                                                                                                                                                                                                                                                                                                                        Mohn W.W., Wilson A.E., Bicho P., Moore E.R.B.; "Physiological and Phylogenetic Diversity of Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas abietaniphila.
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9 (TrEMBLrel. 12, 1
1 (TrEMBLrel. 19, 1
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                                                                                  547 AA;
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                                                                                  58500 MW; 49A627265D7C1A74 CRC64;
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     100.0%;
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[00.0%; Pred. No.
                              4.78;
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           Pred. No.
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                                                                                                                                                                       Tomich M., Herfst C.A., Golden J.W., Mohr C.D.;

"Role of Flagella in Burkholderia cepacia Host Cell Invasion.";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AP453480; AAL65160.1;

InterPro: IPR000067; FlgMring_FLIF.

InterPro: IPR002920; YscJ_FliF.

Pfam; PF01514; YscJ_FliF.

Pfam; PF01504; PS01095; FlGMRINGFLIF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkholderia cepacia (Pseudomonas cepacia).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
4-coumarate--CoA_ligase_4CL1 (EC 6.2.1.12).
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Pfam; PF00501; AMP-binding; 1.
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"Isolation of three 4-coumarate--CoA ligase cDNA homologues from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. ELLET;
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8; Conserv
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                                                                                                                                         TIGR00206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAALSVL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                             62991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60293 MW; 8194EE1B939D2925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                      100.0%;
                                                         4.7%;
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100.0%; Pred. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta
               Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
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                                                                                                                      4B142D53E065CB91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision; Burkholderia group;
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               DB 2;
5. 25;
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ACCOMPAND TO THE PROPERTY OF T
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Query Match
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PRINTS; PR00053; FORKHEAD.

ProDom; PD000425; TF_Fork_head; 1.

SMART; SM00339; FH; 1.

PROSITE; PS00657; FORK, HEAD_1; 1.

PROSITE; PS00658; FORK_HEAD_2; 1.

PROSITE; PS0039; FORK_HEAD_3; 1.

SEQUENCE 587 AA; 64092 MW; 08051
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Musc
                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                         STRAIN-BERKELEY;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                           CG15295 protein. CG15295.
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq.
01-MAY-2000 (TrEMBLrel. 13, Last anno
                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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01-JUL-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001766; TF_Fork_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dorso J.C., Erives A., Di Gregorio A., Chang A., Levine M.;
Dorsoventral patterning of the vertebrate neural tube is conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 QIAAAAAA 87
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100.0%; Pred. N
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Lisk N., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Ra Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhon W., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhong G., Zhao M., Zhu X., Smith H.O.,

RA Zhense, Frannon30720: CC15295.

REMBI, AB003451; AAF46609.1; -.

DR RIVBRSE, FRANNON3601. CC15295.
        PARA A MARA RAA BEERA A MARA A MEBERA BEERA A MARA 
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AMEDILINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards J., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chanpe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9W0E6 PRELIMINARY; PRT; 637 AA.

Q9W0E6; Q9W0E7; Q9U696;

01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Poly-U-binding-splicing-factor protein (CG12085 protein).

PUBSF OR POLY-U-BINDING-SPLICING-FACTOR OR CG12085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidng Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidng Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Sannders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                        RESULT 30
Q8T6B9
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Matches
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmar
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                  OBTGB9;
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
Half pint.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003471; AAF47501.1; -.
EMBL; AE003471; AAF47502.1; -.
EMBL; AF190745; AAF04132.1; -.
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Page McCaw P.S., Amonlirdviman K., Sharp P.A.;

"PUF50: A pyrimidine-tract binding splicing factor and U2AF65 homolog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM_RNP_1; 2.
SEQUENCE 637 AA; 67939 MW;
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                                                                                                                                                        Drosophila melanogaster (Fruit fly)
Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                       Q8T6B9
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                                                                                                                                       NCBI_TaxID=7227;
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(TremBLrel. 21, Last seq
(TremBLrel. 21, Last ann
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                               Last annotation update)
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                                                                                                                                                                                                                                                                                                                                             637 AA.
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o. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 637;
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Fleischmann W.,
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van Buskirk C., Schupbach T.;
"Half pint regulates alternative
Drosophila.";

splice site selection in

EMBL; AF479079; AAL86452.1; Dev. Cell 0:0-0(2002)

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Q9FRV2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
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Q9FRV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.

REMBL; AB049822; BAB20812.1; -.

RINTERPRO; IPR004407; ACCHAC_1g.

RINTERPRO; IPR000399; TPP_enzyme.

Pfam; PF00205; TPP_enzymes; 1.

RPfam; PF002775; TPP_enzymes; 1.

RPfam; PF02776; TPP_enzymes_C; 1.

RPfam; PF02776; TPP_enzymes_C; 1.

RPfam; PF02776; TPP_enzymes_C; 1.

RPfam; PF02776; TPP_enzymes_N; 1.

R TIGREAMS; TIGR00118; acclac_1g; 1.

WF1AVOPTOTEN; Lyase; Thiamine Pyrophosphate.

SEQUENCE 644 AA; 69392 MW; ED626E55F8B89EC9 CRC64;
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Best Local :
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                  STRAIN-CV. KINMAZE;
Shimizu T., Kato Y., Nakayama I., Nakayama K., Fukuda A., Tanaka Y.,
"Isolation and Expression of acetolactate synthase genes from Oryza
sativa.";
                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                              Acetolactate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FRV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FRV2
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (Tremblrel.
01-JUN-2002 (Tremblrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimizu T., Kato Y., Nakayama I., Nakayama K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. KINMAZE;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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100.0%; Pred. No.
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Last annotation update)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                          Tanaka Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Q9V9F7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC
DR
DR
DR
DR
DR
DR
DR
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG10417 protein (LD27655P).
                                                                                                                                                                           Q9V9F7
Q9V9F7;
MEDLINE=20196006; PubMed=10731132;
                          SEQUENCE FROM N.A.
                                                                Ephydroidea;
                                                                   CG10417.
Drosophila melanogaster (Fruit fly).
Tracheata; Hexapoda; Insecta;
Tracheata; Hexapoda; Insecta;
                 STRAIN-BERKELEY
                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                       Nature 407:508-513(2000).
EMBL; AL445065; CAC11825.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   Ruepp A., Graml W., Santos Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004407; Acolac_lg.
InterPro; IPR000399; TPP_enzyme.
Pfam; PF00205; TPP_enzymes; 1.
Pfam; PF002775; TPP_enzymes_C; 1.
Pfam; PF002776; TPP_enzymes_N; 1.
TIGREAMS; TIGR00118; acolac_lg; 1.
Flavoprotein; Lyase; Thiamine pyrophosphate.
SEQUENCE 644 AA; 69345 MW; F873F121A9FD9F99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DSM 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical protein Ta0687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9НКВ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9нкв4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP EMBL; AB049823; BAB20813.1;
                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                   128 LHIQIAAA 135
                                                                                                                                                                                                                                                                         3 LHIQIAAA 10
                                                                                                                                                                                                                                                                                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AAAAAALS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                   651 AA;
                                                                                                                                                                                      PRELIMINARY;
                                                           Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                           protein; Complete proteome.
51 AA; 74410 MW; 5F9E9F1711E7B733 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                          4.7%; Score 8;
100.0%; Pred. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.7%; Score 8;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoplasmata; Thermoplasmatales;
                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                    662 AA.
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                                                                                                                                                                                                                                                                                                          DB 17; Length 651;
o. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                  Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                           0,
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                         0;
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RA Harris N.L., Harvey D., Heimand T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heimand T.J., Wei M.-H., Ibogwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J. Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
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  S A E
                                                                                            RESULT 35
                                                                                                                                                                                                                                                                       Matches
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Mabril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow Desna Bender B.G., Related B.D.,
Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL, GenBank/DDBJ databases. EMBL, AE003787; AAF57333.1; EMBL, AY051748; AAK93172.1; EMBL, BY P35813; 1A6Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0033021; CG10417.
InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C-like.
Pfam; PF00481; PP2C; 1.
Q9QY56;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                  Q9QY56
                                                                                                                                                                                                                                                                                               ocal
                                                                                                                                                                        210
                                                                                                                                                                                                                                                                                                                                                                                              SM00332; PP2Cc; 1.
SM00331; PP2C_SIG; 1.
E; PS01032; PP2C; 1.
                                                                                                                                                                                                                     8 AAAAAALS 15
                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                  Similarity 100.0%;
                                                                                                                                                                        AAAAAALS 217
                                                                                                                                                                                                                                                                                                                                                                              662 AA;
                                                                                                                                                                                                                                                                       Conservative
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            72369 MW; C34171B9B030996E CRC64;
                                                                                                                                                                                                                                                                                                                               4.78;

 Mismatches

                                                                                                                                                                                                                                                                                                    Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                               Length 662;
                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                          Gaps
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ACCOMPAND ACCOMP
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Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                Matches
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001092; HLH_basic.
InterPro; IPR001092; Znf_CZH2.
pfam; PF000996; Zf-CZH2. 10.
SMART; SM00355; Znf_CZH2; 9.
SMART; SM00355; Znf_CZH2; 9.
PROSITE; PS00028; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 6.
PROSITE; PS00028; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS00028; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS00028; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel 13, Last sequence update) 01-JUN-2002 (TrEMBLrel 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF126967; AAF22563.1; HSSP; P15822; 3ZNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Runoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY051905; AAK93329.l:

EMBL; AY051905; AAK93329.l:

EMBSE; FB900037471; Alhambra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:109530; E4f1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lebedeva T.V., Singh A.K.; repression by the murine analog repression of the murine I1-1 beta expression by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q960R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q960R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALHAMBRÁ OR CG1070.
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 AAAAAALS 38
600 AAAAAALS 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                        8 AAAAAALS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            783 AA; 84222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                         824 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor."
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                                                                                                                                                                                                                                         84327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                     100.0%;
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100.0%; Pred. No.
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Last annotation update)
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                                                                                                                                                                                                                                            8313513FFB2F6F94 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 783;
                                                                                                                                                                                    DB 5;
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RESULT 37

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Q8SZW9
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0962D2;
01-DEC-2001 (TIEMBLITEL 19, C1
01-DEC-2001 (TIEMBLITEL 19, L1
01-MAR-2002 (TIEMBLITEL 20, L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Q8SZW9;
01-JUN-2002 (TrEMBLrel. 21, Created)
                               6MZS8ð
                                                                                                                                                                 FlyBase; FBgn0037471; Alhambra.
SEQUENCE 975 AA; 98713 MW;
                                                                                                                                                                                    Mech. Dev. 100:291-301(2001).
EMBL; AY036104; AAK63170.1; -.
                                                                                                                                                                                                                  growth.
                                                                                                                                                                                                                      Bahri S.M., Chia W., Yang X.;
"The Drosophila homolog of human AF10/AF17 leukemia fusion genes
(Dalf) encodes a zinc finger/leucine zipper nuclear protein required
                                                                                                                                                                                                                                                     MEDLINE=21095180; PubMed=11165485; Bahri_S.M., Chia W., Yang X.;
                                                                                                                                                                                                                                                                                                  Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                 Zinc finger/leucine zipper protein DALF isoform C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The Drosophila homolog of AF10 is expressed in a striped pattern throughout blastoderm.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidaa; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
S 8; Conserv
                                                                               600 AAAAAALS 607
                                                                                                    8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AAAAAALS 608
                                                                                                                                                                                                              nervous system for maintaining EVE expression and normal
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                          PRELIMINARY;
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             825 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                        Drosophilidae; Drosophila
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                                                                                                                   100.08; FI.
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                                                                                                                                4.7%; Score 8;
100.0%; Pred. No.
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                       PRT; 1015 AA.
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                                                                                                                                      DB 5; Length 975;
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RX MEDILINE-20195006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Berson R.Y., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bultis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D. Heiman T.J., Hernandez J.R., Houck J.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennisson J.A., Ketchum K.A.,
RA Haris N.L., Barren G.H., Ke Z., Kennisson J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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Q9VI61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GONZALEZ M., GUARTIN H., LI P., LIAO G., FIISE E., GEOTGE R., VUNDOO J., PACLED J., PARAGAS V., PARK S., Phouanenavong S., Wan K., U C., Lewis S.E., Rubin G.M., Celniker S., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

SEQUENCE 1015 AA; 100464 MW; CB24616CF137ACF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Champe M., Chavez C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALHAMBRA.
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Drosophilidae; Drosophila.
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng L.,
RA Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
DR EMBL, AB003672; AAR54055.1; -
DR FlyBase; FBgn0037471; Alhambra.
SQ SEQUENCE 1164 AA; 119469 MW; F49C6BC7394DBB6A CRC64;
SEQUENCE 1164 AA; 119469 MW; F49C6BC7394DBB6A CRC64;
SEQUENCE 1164 AA; 119469 MW; F49C6BC7394DBB6A CRC64;
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Result
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Perfect
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length: 2000000000
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172
1 MMLHIQIAAAAAAL:
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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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PCT-US95-04121-52
US-08-523-2268-42
US-08-521-458B-42
US-08-516-859A-103
US-09-528-706-103
US-09-528-706-103
US-09-5180-524-9
US-08-180-524-9
US-08-975-166-9
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US-09-117-121-39
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US-08-443-129-3
US-08-443-129-3
US-08-443-152-3
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US-08-109-286-690-12
US-08-107-676-30
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US-08-117-676-30
US-08-117-676-30
US-09-161-241-9
US-08-142-439A-7
US-08-142-439A-7
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US-09-568-480-5
US-09-68-1395-1
US-08-159-339A-159
US-08-159-339
Sequence 26, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 14, Appl Sequence 151, App Sequence 152, App Sequence 155, App Sequence 155, App Sequence 156, App Sequence 157, App Sequence 161, App Sequence 161, App Sequence 162, App Sequence 163, App Sequence 164, App Sequence 164, App Sequence 165, App Sequence 165, App Sequence 167, App Sequence 167, App Sequence 168, App Sequence 167, App Sequence 170, App Sequence 171, App Sequence 170, App Sequence 17, App Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 17, Appli Sequen
                                                                                                                                                                                                                                                                                         Sequence 3, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 10, Appli Sequence 11, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 5, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Seque
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RESULT 1 US-08-159-339A-154

ALIGNMENTS

Sequence 154, Patent No. 60

6037135

APPLICANT:

COUNTRY:

CA

ADDRESSEE:

MEDIUM TYPE:

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PCT-US95-04121-52
; Sequence 52, Application PC/TUS9504121
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
FILING DATE: 06-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HLA PRITTLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sette, Alessandro APPLICANT: Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Education CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/159,339A FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                    Local Similarity
les 7; Conserv
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Grey, Howard M.
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100.0%; Pred. No.
ative 0; Mismatci
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  Haptenated Peptides and Uses Thereof 62
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RESULT 2

APPLICANT:

US-08-159-339A-154

MOLECULE TYPE:

TOPOLOGY:

LENGTH:

Matches Query Match Best Local

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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04121-52
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US-08-503-226B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 42, Application US/08503226B
Patent No. 5871945
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Best Local
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APPLICANT: Locker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 466-6010
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,;
FILING DATE: APril 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Calcineurin Inhib
TITLE OF INVENTION: Anchoring Protein
NUMBER OF SEQUENCES: 42
                                                       FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,227
FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,731
FILING DATE: 15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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mes 7; Conservative
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                                                                                                                                                                                                            CLASSIFICATION: 436
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 233 St
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                    FILING DATE:
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233 South Wacker Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lockerbie, Robert Owen, et al. VENTION: Calcineurin Inhibitory Compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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cker Drive, 6300 Sears Tower
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        27866/32861
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Gaps

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US-08-721-458B-42
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                      Query Match
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GENERAL INFORMATION:
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/08721458B Patent No. 6107104
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                                                                                                                                                             INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,227
APPLICATION NUMBER: US 08/344,227
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/503,226
FILING DATE: 17-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-4740448
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC - DOS/MS - DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                  MOLECULE TYPE:
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                               TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lockerbi
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
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LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                 TYPE:
                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                       NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 01 FILING DATE: 15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/721,458B
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                                                                                                          H: 14 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAAL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 South Wacker Drive,
                                                                                                                                                                                 312-4740448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lockerbie, Robert Owen, et al. VENTION: Calcineurin Inhibitory Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marshall, O'Toole, Gerstein, Murray & Borun
3 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312-474-6300
                                                                peptide
                                                                                              single
 4.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Anchoring Protein : 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       US 08/404,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1%; Score 7; DB 2; 100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42:
Score 7;
Pred. No.
                                                                                                                                                                                                                             27866/33276
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 DB 3;
             Length 14;
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Sequence 103, Application US/09586472
PATENT NO. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
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                                                                                                                                                                                 US-09-586-472-103
                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                            US-08-516-859A-103
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US-08-516-859A-103
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 103, Application US/08516859A Patent No. 6069231
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Huang, Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Retinoblastoma Prote:
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                           NUMBER OF SEQUENCES:
                                                                                     TITLE OF INVENTION: Retinoblastoma Protein - Interacting
                                                                                                                                                                                                                                                    6 AAAAAAL 12
                                                                                                                                                                                                                                                                                   8 AAAAAAL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                         22 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                  4.1%; Score 7; DB 3; 100.0%; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/292,683
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                                                                        Finger Proteins
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                                                                                                                                                                                                                                                                                                                                                    Length 22;
                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 103:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 18-AUG-1994
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 9-LJ 4130
TELEPONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 7; Conserv
                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                              COUNTRY: USA
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APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        I: 4370 Là Jolla Village Drive, Suite 700
San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAAL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 7; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                   Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                           Retinoblastoma Protein - Interacting
    US 08/516,859
                                                                                    us/09/528,706
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/409,217

PILING DATE: 19-SEP-1989

ATTORNEY/AGENT INFORMATION:

NAME: KTYSHAK, Thad

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 66-005-9234-1

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                          APPLICATION NUMBER: FILING DATE: 28-FEB
                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Milwaukee
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Bower, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodes, Thomas
Huige, Nick
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Lusk, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicoye, Etzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thad Kryshak, Quarles & Brady
                                                                                                                                            28-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edward
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                                                                                                                                                                US 07/486,333
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                                                                                                                                                                                                   US/07/917,216
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o. 3.6;
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US-08-180-524-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                      APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
RECISTRATION NUMBER: 35,433
RECISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 7; Conserv
TELEFAX: (414) 277-559 INFORMATION FOR SEQ ID NO:
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                REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEPAX: (414) 277-5591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: |
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/180,524 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 411 Eas
CITY: Milwaukee
STATE: Wisconsi
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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5849537
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Huige, Nick
Kot, Edward
Chicoye, Etzer
Barney, Michael C.
Bower, Patricia A.
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Rhodes, Thomas
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100.0%; Pr
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                                                              66-005-9234-1
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Pred. No.
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PRICE APPLICATION NUMBER: US 07/409,217
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-92
TELEPHONE: (414) 277-5707
TELEPHONE: (414) 277-5591
TELEFAX: (414) 277-5591
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US-08-180-524-9
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APPLICANT: Tripp, I
APPLICANT: Lusk, La
APPLICANT: Rhodes,
APPLICANT: Huige, I
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SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%; Pred. No. hes 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Milwaukee
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411 East Wisconsin Avenue
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Huige, Nick
Kot, Edward
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Barney, Michael C.
Bower, Patricia A.
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TOPOLOGY: linear

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; MOLECULE TYPE:
; HYPOTHETICAL: N
; ANTI-SENSE: NO
US-08-180-524-9
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                                                                                                              TELEFAX: (414) 277-5591 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cronan, Charles I.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                            REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ADDRESSEE: Thad Kryshak, Quarles & Brady
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                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
                                                                                                                                                                                                                                                   FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
HYPOTHETICAL:
              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Milwaukee
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                                              LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                  TOPOLOGY:
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7; Conserva
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Barney, Michael C.
Bower, Patricia A.
                             ະSS: single
linear
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Huige, Nick
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                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%; Score 7; DB:
100.0%; Pred. No. 6;
tive 0; Mismatches
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                                                                                                                                                                                                                                                           US 07/409,217
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US-08-975-166-8
US-08-975-166-8
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Best Local Similarity 100.0%; Pred. No. v,

Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/486,333

FILING DATE: 28-FEB-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217

FILING DATE: 19-SEP-1989

ATTORNEY/AGENT INFORMATION:
NAME: KLYSDAK, Thad
REGISTRATION NUMBER: 35,433

REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                   TELEFAX: (414) 277-55
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                 ANTI-SENSE:
                                                                                                                                 SEQUENCE CHARACTERISTICS:
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OTTY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: MSWORD Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                  TELEPHONE:
                                                                                                                LENGTH:
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                                                                                                amino acid
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                                                                                                              37 amino acids
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                 NO
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                                                                 linear
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                                                                               single
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                                                                                                                                                                                       277-5707
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; ANTI-SENSE:
US-08-975-166-9
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US-08-975-166-9
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNIA...
ZIP: 53202
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOMPUTER: IBM PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Apprication 5928877
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                           MOLECULE TYPE:
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOTTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                             TOPOLOGY:
                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                              NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/917,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Milwaukee
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Huige, Nick
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                                                                                                             linear
                                                                                  NO
                                                                                                                           single
                                                                                               protein
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100.08;
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   100.0%;
                   4.18;
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Score 7; Pred. No.
                                                                                                                                                                                                                                                    66-005-9234-1
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Pred. No.
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DB 2;
o. 6;
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; Patent No.
                                                                                                       RESULT 15
US-09-117-121-42
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; OTHER INFORMATION:
US-09-117-121-39
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US-09-117-121-39
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                                                                        Sequence 42, Application US/09117121 Patent No. 6307020
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                               Query Match
GENERAL INFORMATION:
APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. GRANTION:
GENERAL INFORMATION:
APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Anti
TITLE OF INVENTION: and Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PO
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,6
                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-NOV-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                 Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                    6 AAAAAAL 12
                                                                                                                                                                                                  8 AAAAAAL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576-0300
                                                                                                                                                                                                                             4.1%; Score 7; DB 4;
100.0%; Pred. No. 6;
1tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Intracellular Antifreeze Polypeptides
                                                                                                                                                                                                                                                                                                              /note= "HPLC-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO PCT/CA97/00062
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                                                                                                                                                                                                                                                            Length 37;
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                                                                                                                                                                                                                           0;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

Two Embarcadero Center, Eighth Floor

Townsend and Townsend and Crew LLP

TITLE OF INVENTION: NUMBER OF SEQUENCES:

and Nucleic Acids

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US-09-344-529-4
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                                                          US-09-344-529-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09344529 Patent No. 6429293
                                                                                                                                                                              SEQ ID NO 4
LENGTH: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
               Query Match
                                                                                                                                                                                                                                                                                                         APPLICANT: Hew, Choy L.
APPLICANT: HSC Research and Development Limited Partnership
APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
FILE REFERENCE: 016252-002620US
FILE REFERENCE: 016252-002620US
CURRENT APPLICATION NUMBER: US/99/344,529
CURRENT FILING DATE: 1999-06-24
EARLIER APPLICATION NUMBER: US 60/090,794
EARLIER FILING DATE: 1998-06-26
EARLIER FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: US 60/095,713
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
                                                                          OTHER INFORMATION: Winter flounder liver-type antifreeze polypeptide OTHER INFORMATION: (wflafP-6)
                                                                                                                        FEATURE:
                                                                                                                                         ORGANISM: Pleuronectes americanus
                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/G
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarcas
CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No.
ative 0; Mismatc
4.1%;
100.0%;
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Score 7; DB 4; Pred. No. 6;
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                   Length 37
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Best Local Similarity
has 7; Conserve
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                                                                                                                                          US-07-812-421-1
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                                                                                                                                                             RESULT 18
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                                                                                                        Sequence 1, Application US/07812421 Patent No. 5932697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
EFILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 1:
APPLICANT: Caceci, APPLICANT: Toth, The APPLICANT: Szumansk: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: WHITHAM, CURTIS & WHITHAM STREET: Reston Intl. Center, 11800 Sunrise Valley Dr., STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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     Szumanski, Maria B.W.
VENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
VENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
                                                      Toth, Thomas E.
                                                                                                                                                                                                                                                                                     Conservative
                                                                     Caceci, Thomas
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                                                                                                                                                                                                                                                                                                      4.1%; Score 7; DB 2;
[00.0%; Pred. No. 6.1;
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 Mismatches

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NUMBER OF SEQUENCES:

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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 144
LENGTH: 109
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-325-932A-144
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                               Ω
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Anne-
                                                                 Matches
                                                                                               Query Match
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TITLE OF INVENITION: Compositions affecting programmed cell
TITLE OF INVENITION: death and their use in the modification of forestry plant develo
                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-391-9035 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/ACENT INFORMATION:
NAME: Whitham, Michael E.
DECTERDATION NUMBER: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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18 AAAAAAL 24
                             8 AAAAAAL 14
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                                                                            h 4.18;
Similarity 100.08;
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                                                              Conservative
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ilarity 100.0%; Pred. No.
Conservative 0; Mismatcl
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RESTON Intl. Center, 11800 Sunrise Valley Dr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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23-DEC-1991
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                                                            0;
                                                                          Score 7; ; Pred. No.
                                                          Mismatches
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                                                                                         DB 4;
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                                                                                        Length 109;
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US-08-444-083-3
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US-08-233-609-3
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Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatch
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Patent No. 5534615
                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                         APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                   APPLICANT: Baker, Joffre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Joffre APPLICANT: Chien, Kenneth APPLICANT: King, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pennica, Diane APPLICANT: Wood, William
CITY: South San Francisco
                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: South San Francisco
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                                                                                                                                                                                                                                                                                                                                          91 AAALSVL 97
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               E: Genentech, Inc.
460 Point San Bruno Blvd
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lo. 31;
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COUNTRY:

USA

94080

STATE: California

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US-08-444-083-3
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US-08-286-304-3
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Best Local Similarity luv.
"---hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 3, Application US/08286304
Patent No. 5571893
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
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FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/21 FILING DATE: 05-AUG-1994 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,304
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pennica, Diane APPLICANT: Wood, William
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 25-APR-1994
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                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                   94080
                                                                                                                                                                                                                                                                                      SSEE: Genentech, Inc.
T: 460 Point San Bruno Blvd
South San Francisco
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                                                                                                                                                                                                                                                                      California
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King, Kathleen
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100.0%; Pred. No. 31;
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                      08/233609
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US-08-442-745-3
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NAME: HASAK, JARDET E.
REGISTRATION UNMBER: 28,616
REFERENCE/DOCKET NUMBER: 894P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
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                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,745
FILING DATE: 17-may-1995
FILING DATE: 17-may-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
                                                                                                                                               REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                        FILING DATE: 25-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                APPLICATION NUMBER: 08/28
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 203 amino acids TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/233609 FILING DATE: 25-APR-1994
                                      TYPE:
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TELEX: 910/371-7168
                                                                                                                                                                                                              REGISTRATION NUMBER:
                  TOPOLOGY:
                                                      LENGTH:
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                                  amino acids
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                                                                                                                                   415/952-9881
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                    linear
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05-AUG-1994
                                                                                                                                                                                           36,700
ER: 894P1D1
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RESULT 25
US-08-443-952-3
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
I-RNGTH: 203 amino acids
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             Sequence 3, Application US/08443952
                                                                                                                                                 Query Match 4.1%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 31; Matches 7; Conservative 0; Mismatches
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Best Local Similarity
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/233609
APPLICATION NUMBER: 25-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/2 FILING DATE: 05-AUG-1994 PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: (null)
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blyd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415/252-9881
                                                                                                                                                                                                                                                                                                                                                                            NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08 FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 304
                                                                                                                        11 AAALSVL 17
                                                                                           91 AAALSVL 97
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Chien, Kenneth
King, Kathleen
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Best Local 9
                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                            CORRESPONDENCE ADDRESS
                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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 STATE:
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                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                                                                     91 AAALSVL 97
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California
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; Sequence 3, Application US/08443130
; Patent No. 5723585
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FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           APPLICANT: King, Kathleen APPLICANT: Pennica, Diane APPLICANT: Wood, William APPLICANT: "The control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Joffre APPLICANT: Chien, Kenneth APPLICANT: King, Kathleen
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                                                                                                                                                                                                                                                   TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 203 amino acids TYPE: amino acid
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                                                                                                              Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.1%; Score 7; DB 1; 100.0%; Pred. No. 31;
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 Mismatches

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RESULT 27
US-08-898-911-3
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CCLASSIFICATION DATA:
APPLICATION NUMBER: 08/233609
EILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
EILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894PlD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEPHONE: 415/057.777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, Timothy E.
REGISTRATION. NUMBER: 36,7
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: \boldsymbol{8}
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                  FILING DATE: 05-AUG-
PRIOR APPLICATION DATA:
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TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                   CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                  APPLICATION NUMBER: US/08/898,911 FILING DATE: 23-Jul-1997
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Local Similarity 100.0%; Pred. No. 31;
es 7; Conservative 0; Mismatches
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                  94080
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                                     05-AUG-1994
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08/452555
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QY
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                  Matches
                                                              Query Match
                                                                                                                                                                                   TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delrdre L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb:
COMPUTER: IBM PC compatible
OPERATIKG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
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                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids:
TYPE: amino acid
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 25-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 203 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Conley, Deirdre L. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                   TELEPHONE: 415/225-18
TELEFAX: 415/952-9881
TELEX: 910/371-7168
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                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                               Local Similarity
les 7; Conserv
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     11 AAALSVL 17
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                                    Conservative
                                                                                                                    linear
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            4.1%; 50.
/ 100.0%; Pred. No. .
0; Mismatches
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100.0%; Pred. No. 31;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 Kb floppy disk
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                                                    Score 7; DB 5; pred. No. 31;
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91 AAALSVL 97

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US-08-508-761B-32
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Best Local Similarity
"atches 7; Conserve
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; ORGANISM: Fibrobacter succinogenes
US-09-286-690-12
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CURRENT APPLICATION NUMBER: US/09/286,690
CURRENT FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,882
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/US97/17811
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 12
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SEQ ID NO 12
LENGTH: 228
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APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
             NAME: Player William E.
REGISTRATION NUMBER: 31.409
REFERENCE/DOCKET NUMBER: P58525NA
TELECOMMUNICATION INFORMATION:
                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91/09870
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: System for Protein Expression and TITLE OF INVENTION: Secretion Especially in Corynebacteria NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Duchiron, Fran
APPLICANT: Renaud, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Joliff, Gwennael APPLICANT: Guyonvarch, Arme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                 APPLICATION NUMBER: FR 91/09652 FILING DATE: 29-JUL-1991
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/508,761B
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duchiron, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guyonvarch, Armel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purification, Relano
                                                                                                                                                                                                                                                                                                IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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(202) 638-6666
                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                         31-JUL-1995
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RESULT 31
US-08-107-676-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/08107676 Patent No. 5955356
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                                                                                                                                                     INFORMATION FOR SEQ ID NO: 30:
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                              IMMEDIATE SOURCE:
                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                             FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91400388.4
                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                 FILING DATE: 14-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DeWit, Lucas
APPLICANT: DeBruyn, Jacqueline
TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding Them for Diagnosis and Control of
TITLE OF INVENTION: Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
 CLONE:
                CLONE:
                                                                                          TOPOLOGY: linear
                                                                                                                       LENGTH:
                                          ORGANISM: Mycobacterium kansasii
                                                                                                             TYPE:
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/EP92/00268
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 04-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 310
                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: M. kansaii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AAAAAAL 14
                                                                                                        amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AAAAAAL 9
                                                                                                                                                                                                                                                Kowalchyk, Katherine M.
from M.kansasii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
     Partial protein sequence from antigen 85B
                                                                                                                                                                        612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3100 No. 5955356west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 amino acids
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DeWit, Lucas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merchant & Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 7; DB 3; 100.0%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                         US/08/107,676
                                                                                                                                                                                                                                  36,848
                                                                                                                                                                                                                   8076.89USWO

 Mismatches

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RESULT 32
US-09-161-241-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/07792885A Patent No. 5516651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: A-548
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TYPE: PRT
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                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goldring, Steven R.
APPLICANT: Gorn, Alan H.
APPLICANT: Lin, Herb Y.
TITLE OF INVENTION: MAMMALIAN CALCITONIN RECEPTOR
NUMBER OF SEQUENCES: 2
                                                                                APPLICATION NUMBER: US FILING DATE: 19911115 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,1
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                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                          CITY:
                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                          ZIP:
                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 AAAAAAL 344
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02110-2804
                                                                                                                                                                                                                                                                                                          Boston
                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                            225 Franklin Street
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                                                                                                                                       US/07/792,885A
     30,162
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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); ORGANISM:
US-08-142-439A-7
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GENERAL INFORMATION:
APPLICATION:
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Best Local :
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                     TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thorens, Bernard TITLE OF INVENTION: Receptor TITLE OF INVENTION: (GLP-1) NUMBER OF SEQUENCES: 9
                                                                                STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE: 25-MAR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.1%; Score 7; Local Similarity 100.0%; Pred. No. es 7; Conservative 0; Mismathus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                         NAME: Harrington, James J. REGISTRATION NUMBER: 38,71
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/142,439A FILING DATE: 24-NOV-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 AAAAAAL 437
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                                                                                                                                      amino acid
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                                                                                                                                                      482 amino acids
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                                                                                                         linear
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                   Sus scrofa
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                                                                                      protein
                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                                                 PCT/EP93/00697
                                                                                                                                                                                                                                                                                                                                                                                                  DK 398/92
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5. 72;
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RESULT 36
US-09-172-952-26
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US-08-869-477-7
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                                                                                                                                                Matches
                                                                                                                                                           Query Match
Best Local 9
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                  MOLECULE TYPE: p
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 24-NOV-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DK 398/92 FILING DATE: 25-MAR-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
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                                                                            431 AAAAAAL 437
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10174-6201
                                                                                                                                            Similarity 100. 7; Conservative
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                                                                                                           AAAAAAL 14
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                                                                                                                                                                                                                                                                                                                                                                       482 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 58467470 No. 5846747disk of No. 5846747th America, Inc.
                                                                                                                                                                                                                                                                                       NO
                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                        single
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100.0%; Pred. No. 72
tive 0; Mismatches
                                                                                                                                          4.1%; Score 7; DB
100.0%; Pred. No. 72
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor for the Glucagon-Like-Peptide-1 (GLP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bernard
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                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                           Length 482;
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US-09-382-256-10
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US-09-172-952-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application Patent No. 6207814
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 498
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REFERENCE: 234/191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES,
HAVING SERINE THREONINE KINASE
AND THEIR USE
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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ADDRESSEE: Fulbright & Jaworski L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MIYAZONO, Kohei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 YNMSLGE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 YNMSLGE 122
APPLICATION NUMBER: GB 9304680.:
PILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 331344.5
FILING DATE: October 15, 1993
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/382,256A FILING DATE: 24-Aug-1999 CLASSIFICATION: 514
                                                                                                                                                                       APPLICATION NUMBER: GB 9224057.1 FILING DATE: No. 6207814ember 17, APPLICATION NUMBER: GB 9304677.9 FILING DATE: March 8, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York City
STATE: New York
                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/GB93/02367 FILING DATE: No. 6207814ember 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEN DIJKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                         GB 9304680.3
                                                                                                                                                                                                                                                                                                                                                                                                                          3.25 inch, 1.44mb
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RESULT 38
US-09-395-115-10
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ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                              APPLICATION NUMBER: 9304677.9 FILING DATE: 8-March-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                    PRIOR APPLICATION DATA:
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                   FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
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                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                               APPLICATION NUMBER: 93110 FILING DATE: 28-May-1993
                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York City
APPLICATION NUMBER:
                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: No. 6207814man D. Han REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: LUD 5298.1
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                                      2-July-1993
                                                                                                                                                                                                                                                                                                                                                                     JMBER: US/08/436,265
30-October-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 3.5 inch, 360 kb storage
                                                            9313763.6
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                                                                                                                                                                             9304680.3
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Pred. No.
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Best Local
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                                                                                                             FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
9311047.6
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
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LENGTH: 503 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-October-
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                 PRIOR APPLICATION DATA:
                                                                              APPLICATION NUMBER: FILING DATE: 28-May-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Miyazono, APPLICANT: Franzen, I
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/43 FILING DATE: 30-October-1995 CLASSIFICATION: 435
                                                  FILING DATE:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: 9224057.1 FILING DATE: 17-No. 6316217ember-1992
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/GB93/02367 FILING DATE: 17-No. 6316217ember-1993
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                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
APPLICATION NUMBER: 913609 FILING DATE: 3-August-1993
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Similarity 100.0%;
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805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                       Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (212) 688-92
(212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-October-1993
                                                2-July-1993
                                                                                                   28-May-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Kohei; Dijke, Peter Ten;
Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
Activin Receptor-Like Kinase, Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Having Serine Threonine Kinase Domains And Their Use
                                                                   9313763
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RESULT 40
US-09-679-187-10
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// TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-436-265-10

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SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
                                                FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
                                                                                                                                      APPLICATION NUMBER: 9304680.3
FILING DATE: 2-July-1993 PRIOR APPLICATION DATA:
                                                                                                        FILING DATE: 8-March-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                              APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/430 FILING DATE: 30-October-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cli.
STATE: Ne.
10022
                  APPLICATION NUMBER: FILING DATE: 2-July
                                                                                      APPLICATION NUMBER: 9311047.6
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SOFTWARE: Wordper
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REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
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FILING DATE: 15-October-1993
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(212) 838-3884
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                                                                                      Query Match
Best Local :
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TELEFAX: (212) 838-3884
INFORMATION FOR EGO ID NO: 10-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      TYPE: amino acids
TOPOLOGY: linc-
MOLECHIE TYPE: TYPE: Amino acid
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-October-1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 9136099.2 FILING DATE: 3-August-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: 9321344.5
                                                            / Match 4.1%; Score 7; DB 4; Local Similarity 100.0%; Pred. No. 75; hes 7; Conservative 0; Mismatches
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21 AAAAAAL 27
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Search completed: July 6, 2003, 14:22:34 Job time: 21 secs

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Maximum DB seq length: 2000000000
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                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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. /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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US-09-9864-761-40439
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US-09-9864-761-770
US-10-92-1544-770
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US-09-764-891-7737
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US-09-764-891-787-790
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US-09-164-615-49
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          Sequence 25, Appl Sequence 7, Appl Sequence 7, Appl Sequence 165, App Sequence 104, Appl Sequence 10, Appl Sequence 770, App Sequence 770, App Sequence 2737, App Sequence 2737, App Sequence 2737, App Sequence 44, Appl Sequence 43, Appl Sequence 43, Appl Sequence 3, Appli Sequence 3, Appli
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Sequence 9684, Ap

Sequence 12279, A

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Sequence 236, Appli

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; ORGANISM: Drosophila melanogaster US-10-108-605-25
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US-09-864-761-42679
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                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42679, Application US/09864761 Patent No. US20020048763A1
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Best Local
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APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR APPLICATION DATE: 2001-01-16
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                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-x-1 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/176,418 PRIOR FILING DATE: 2000-01-14 NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                               PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                  APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng
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             APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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8; Conserv
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Bachmann, Jane
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NUMBER: PCT/US01/00666
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US-10-223-083-50

US-09-909-320-236

US-09-909-088B-236

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Sequence 236, App
Sequence 8, Appli
Sequence 4875, Ap
Sequence 10782, A
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Sequence 50, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10024450 Publication No. US20030032606A1
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Best Local
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                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7 \,
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                            APPLICANT: Huang, Shi
APPLICANT: Chadwick, Robert B.
TITLE OF INVENTION: Methods of Detecting and Treating
TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using
FILE REFERENCE: P-LJ 5101
FILE REFERENCE: P-LJ 5101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
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                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/024,450 CURRENT FILING DATE: 2001-12-17 PRIOR APPLICATION NUMBER: US 60/256,582 PRIOR FILING DATE: 2000-12-19
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NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.86

OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 0.86

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 1.4
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                   LENGTH: 21
TYPE: PRT
                                                                                                              NUMBER OF SEQ ID NOS: 15
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
FILING DATE: 1001-01-30
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
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00.0%; Pred. No.
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Publication No. US20030121065A1
GENERAL INFORMATION:
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SEQ ID NO 29
LENGTH: 23
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TITLE OF INVENTION: 64 Human Secreted Proteins
FILE REFERENCE: PZ011
CURRENT APPLICATION NUMBER: US/09/776,724A
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/180,909
                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 09/669,688
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 09/229,982
PRIOR FILING DATE: 1999-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MULTIFUNCTIONAL BASE SEQUENCE AND ARTIFICIAL GENE CONTAINING THE FILE REFERENCE: 4439-4004
CURRENT APPLICATION NUMBER: US/10/311,111
CURRENT FILING DATE: 2002-12-13
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                                                                                         PRIOR
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                                                                 FILING DATE: 1997-07-16
APPLICATION NUMBER: 60/052,874
FILING DATE: 1997-07-16
                                                                                                                                                                          APPLICATION NUMBER: 60/052,661 FILING DATE: 1997-07-16
                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US98/14613 FILING DATE: 1998-07-15
                                 APPLICATION NUMBER: 60/052,873 FILING DATE: 1997-07-16
                                                                                                                     FILING DATE: 1997-07-16
APPLICATION NUMBER: 60/052,871
                                                                                                                                        APPLICATION NUMBER: 60/052,872 FILING DATE: 1997-07-16
APPLICATION NUMBER: 60/052,870 FILING DATE: 1997-07-16
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; ORGANISM: Hepatitis US-10-106-487-1
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US-10-106-487-1
                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
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LENGTH: 38
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APPLICANT: LANGLADE-DEMOYEN, PIERRE
APPLICANT: MICHEL, MARIE-LOUISE
PITLE OF INVENTION: DESIGN OF A POLYEPITOPIC CONSTRUCT FOR THE INDUCTION
TITLE OF INVENTION: OF
TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
TITLE OF INVENTION: HLD MICE
FILE REFERENCE: 03495.0196 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/106,487
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: MINISTERN AND ACTE 673
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APPLICANT: FIRAT, H
APPLICANT: LEMONNI
                                                                                                                                                 NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/158,356
PRIOR FILING DATE: 1999-10-12
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/675,673
PRIOR FILING DATE: 2000-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/053,442
                                                                     TYPE: PRT
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                                                                                            LENGTH:
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CONTROL DATE: 1997-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/055,724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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100.0%; Pred. No. 26;
 4.1%;
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Length 41;
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 40439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
OTHER INFORMATION: MAP TO AL121747.19
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/608,408
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1 ; OTHER INFORMATION: EST_HUMAN HIT: AU131227.1, EVALUE 3.00e-05 US-09-864-761-40439
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                                                                       US-10-092-154-770
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 770, Applic Publication No. US20 GENERAL INFORMATION:
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LENGTH: 78
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020042098A1 GENERAL INFORMATION:
                                                                                                                                                                                                              SEQ ID NO 770
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Best Local Similarity Matches 7; Conserv
                                Query Match
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CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,755
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32253 TRANSPERASE FAMILY MEMBERS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 38155-20004.00
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2003
Prior Application removed
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                           LENGTH: 79
                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                       OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                         FEATURE:
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                                                                                                        LOCATION: (73)
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100.0%; Pred. No.
                4.18;
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                  Score 7; 1; Pred. No.
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lo. 35;
                    DB 9;
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                                  Length 79;
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RESULT 12
US-09-764-891-2737
; Sequence 2737, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                   US-10-219-220-144
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; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-770
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US-09-764-847-770
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 144, Application US/10219220 Publication No. US20030082724A1 GENERAL INFORMATION:
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Compositions affecting programmed cell TITLE OF INVENTION: death and their use in the modification of the Reference: 11000.1022c1 CURRENT APPLICATION NUMBER: US/10/219,220 CURRENT FILING DATE: 2002-08-14 PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932 PRIOR FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Flinn, Barry APPLICANT: Lasham, Anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                           ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
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100.0%; Pred. No.
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Pred. No.
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APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Settlage, Sharon
TITLE OF INVENTION: Geminivirus Resistant Transgenic Plants
FILE REFERENCE: 5051-433
CURRENT APPLICATION NUMBER: US/09/164,615B
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
LENGTH: 132
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                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                           Sequence 49, Application US/09164615B Patent No. US20020073442A1
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LENGTH: 131
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CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: SettLage, Sharon
TITLE OF INVENTION: Geminivirus Resistant Transgenic Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 5051-433
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OTHER INFORMATION: Description of Artificial Sequence: TYCLV mutant
OTHER INFORMATION: C3 (mC3#67)
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: SITE
LOCATION: (103)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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nes 7; Conserv
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100.0%; Pred. No.
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5. 73;
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; OTHER INFORMATION: Description of Artificial Sequence: TGMV ; OTHER INFORMATION: mutant (mAL3#67) US-09-164-615-49
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US-09-864-761-42364
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PRIOR FILING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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Patent No. US20020048763A1
GENERAL INFORMATION:
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                                      SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 42364
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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PRIOR
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                       PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: US 09/774,203
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                                                                                                  PRIOR FILING DATE:
                                                                                NUMBER OF SEQ ID NOS: 49117
TYPE: PRT
                      LENGTH:
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nes 7; Conserv
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APPLICATION NUMBER: PCT/US01/00670
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                    APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00661
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100.0%; Pr
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APPLICANT: Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN
TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses th
FILE REFERENCE: 77813-37
FULL REFERENCE: 77813-37
CURRENT APPLICATION NUMBER: US/09/747,348
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/171,525
PRIOR FILING DATE: 1999-12-22
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US-10-107-931-3
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Publication No. US20030054550A1
GENERAL INFORMATION:
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Best Local :
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Best Local Similarity
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

OTHER INFORMATION: SWISSPROT HIT: P11227, EVALUE 9.00e-14

OTHER INFORMATION: EXTENSIBLE OF THE STANDARD STAND
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                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: \boldsymbol{8}
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COMPUTER: IBM PC compatible
                                                                                                                                    COUNTRY:
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King, Kathleen
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100.0%; F1
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100.0%; Pred. No.
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Pred. No.

 Mismatches

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o. 96;
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o. 1.1e+02;
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US-09-896-856-3
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,856
FILING DATE: 29-Jun-2001
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                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
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LENGTH: 203 amino acids
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FILING DATE: 30-Jul-1999
APPLICATION NUMBER: 08/286,304
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/10/107,931

EILING DATE: 26-Mar-2002

CLASSIFICATION: <Unknown>
                          APPLICATION NUMBER: US 08/733,850
FILLING DATE: 18-OCT-1996
APPLICATION NUMBER: US 08/471,112
FILLING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/233,609
FILLING DATE: 25-APR-1994
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FILING DATE: 05-AUG-1994
                  APPLICATION NUMBER: 08/286304
                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
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King, Kathleen
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100.08; Pr
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o. 1.2e+02;
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US-09-864-761-36691
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Patent No. US20020048763A1
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APPLICANT:
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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                        APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
        APPLICATION NUMBER: US 60/234,687
                                                                                                                                               APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                                                                                           FILING DATE: 2001-01-30
                                                                                                                            APPLICATION NUMBER: PCT/US01/00662
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REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P0894P1D2C1
TELECOMMUNICATION INFORMATION:
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FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
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LENGTH: 203 amino acids
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TELEX: 910/371-7168
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2000-09-21
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100.0%; Pred. No.
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OTHER INFORMATION: MAP TO AC006460.2

OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEALT, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BJ011 LIVER, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BOLLY EXPRESSED IN BOLLY EXPRESSED IN BOLLY SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BOLLY MARROW, SIGNAL = 1.8

OTHER INFORMATION: SWISSPROT HIT: Q62722, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AU131373.1, EVALUE 1.00e-114
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RESULT 21
US-10-156-761-12279
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                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptomyces avermitilis US-10-156-761-9684
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36691
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Best Local Similarity 100.0%;
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PRIOR FILING DATE: 2000-06-30
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SED ID NOS: 15109
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                                                                                                   157 AAAAAAL 163
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; Pred. No. 1.6e+02;

 Mismatches

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o. 1.5e+02;
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FILE REFERENCE: 249-262

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR ETLING DATE: 2001-08-02

NUMBER OF SEG ID NOS: 15109

SEQ ID NO 9015

LENGTH: 319
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PRIOR FILLING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12279
LENGTH: 300
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Publication No. US20030119018A1
GENERAL INFORMATION:
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                           Matches
                                                                                                         Query Match
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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                                                                                                                                                                                      TYPE: PRT
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301 AAAAALS 307
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                                     · 9 AAAAALS 15
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SAKAKI, YOSHIYUKI
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HORIKAWA, HIROSHI
                                                                             4.1%; Score 7; DB 9; Le
100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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1.7e+02;
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; Sequence 15, Application US/10281024

RESULT 23 US-10-281-024-15

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RESULT 25
US-09-905-291A-236
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US-10-156-761-9858
                                      Sequence 236, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION:
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US-10-281-024-15
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
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LENGTH: 340
       APPLICANT: Genentech, Inc
APPLICANT: Ashkenazi, Av:
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SEQ ID NO 15
LENGTH: 324
TYPE: PRT
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15109
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CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US/09/674,337A
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: PCT/JP99/02305
PRIOR FILING DATE: 1999-04-30
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APPLICANT: Kyoko Higuc
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les 7; Conservative
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     Ashkenazi, Avi
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HORIKAWA, HIROSHI
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o. 1.9e+02;
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o. 1.8e+02;
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                                                                               ; ORGANISM: Homo sapiens US-09-905-291A-236
         Matches
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SEQ ID NO 236
Query Match 4.1%; Score 7; 1
Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatc)
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US00/00219
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PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
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                                                                                                                  TYPE: PRT
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                                                                                                                                    LENGTH:
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FILING DATE: 1999-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US99/21090
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney, Austin L.
Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
                                                                                                                                                                                        2000-01-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09976736 Patent No. US20020161178A1 GENERAL INFORMATION:
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                                                                                                                                    ORGANISM: Homo Sapien US-10-063-547-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/976,736
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US/09/161,241
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 8, Application US/10063547
Publication No. US20020182638A1
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APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                  Matches
                                                                                                                                                                                                          SEQ ID NO 8
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                        APPLICANT: WOOd, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
                                                                                                                                                                                                                                     Prior Application removed -
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
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ORGANISM: Human
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 170
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                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                     LENGTH: 350
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                                                                Local Similarity 100.0%; Pes 7; Conservative 0;
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338 AAAAAAL 344
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                               8 AAAAAAL 14
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Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                             Grimaldi, Christopher J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                  Watanabe, Colin K.
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                                                                                                      4.1%;
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                                                                   Score 7; DB 9; Lei; pred. No. 1.9e+02; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
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                       NUMBER OF SEQ ID NOS: 423
SEQ ID NO 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
                                                                                                   PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1999-11-30
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ENGTH:
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Botstein, David
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Filvaroff, Ellen
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28364
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                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR EILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1999-09-13
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
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CURRENT FILING DATE: 2001-07-17
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08
FILING DATE: 1999-12-02
                                                                                                                                                                           APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15
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Williams, P. Mickey
Wood, William, I.
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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D. US20020197671A1
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f, Ellen
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100.0%; Pred. No.
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o. 1.9e+02;
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
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CURRENT FILING DATE: 2001-11-20
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Best Local Similarity
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TYPE: PRT
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FILING DATE: 1999-09-13
           APPLICATION NUMBER: PCT/US99/20944
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-841-236
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LENGTH: 350
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR EILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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CURRENT FILING DATE: 2001-07-11
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                                                 PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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                APPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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Wood, William, I.
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Eaton, Dan L.
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Botstein, David
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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o. US20030003530A1
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Tumas, Daniel
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100.0%; Pred. No.
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No. 1.9e+02;
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PRIOR ETLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28364
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
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                                                                                                                                                                              ORGANISM: Homo sapiens
US-10-201-310-2
                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 350
TYPE: PRT
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Best Local 9
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LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Soppet, Daniel R.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANTION: Corebellum and Emrbyo Specific Protein
FILE REFERENCE: 1488.061002
CURRENT APPLICATION NUMBER: US/10/201,310
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: US 60/033,870
PRIOR FILING DATE: 1996-12-20
PRIOR FILING DATE: 1996-12-20
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
                                                                                                                               Query Match
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                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
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                                                                                                              Local
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FILING DATE: 1999-12-20
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  338 AAAAAAL 344
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                                            8 AAAAAAL 14
                                                                                    Similarity 100.0%;
7; Conservative
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100.0%; Pred. No.
rative 0; Mismatch
                                                                                                                 4.1%; Score 7; DB 9; Le 100.0%; Pred. No. 1.9e+02;
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o. 1.9e+02;
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RESULT 33 US-10-063-616-8

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RESULT 34
US-09-906-742-236
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CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR ETILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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                                                                                              TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: 10466-14
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APPLICANT: Filvaroff, El
APPLICANT: Gerritsen, Ma
APPLICANT: Goddwrd, Audr
APPLICANT: Godowski, Pau
APPLICANT: Grimaldi, Chr
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APPLICANT:
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LENGTH: 350
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Publication No. US20030013855A1
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo Sapien
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                                                                                                                                              Williams, P. Mickey Wood, William, I.
                                                                                                                                                                                Tumas, Daniel
                                                                                                                                                                                          Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                             Paoni,
                                                                                                                                                                                                                                                                                       Gurney, Austin L. Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                         Kljavin,
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Eaton, Dan L.
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Filvaroff, Ellen
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Botstein, David
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                                                                                                                                                                                                                                                James
                                                                                                                                                                                                                                                                                                                                                                                                   Wei-Qiang
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                                                                                                                                                                                                                            Nicholas F.
                                                                                                                                                                                                                                                                             Ivar J.
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                                                                  SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10063502 Publication No. US20030023042A1 GENERAL INFORMATION:
                                                                                                                                                   APPLICANT: Grimaldi,Christopher J.
APPLICANT: Gurney,Austin L.
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES /
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P0320RIC1
FILE REFERENCE: P0320RIC1
                                                                                                         CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrap
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Goddwski, Paul J.
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SEQ ID NO 236
LENGTH: 350
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                                                                                        NUMBER OF SEQ ID NOS: 170
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
                                              LENGTH: 350
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PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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PRIOR APPLICATION NUMBER: PCT,
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
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                                                                                                  See File Wrapper or Palm
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Matches 7; Conserv
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/905,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR FILING DATE: 1999-09-15
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                                                    APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/28565
                APPLICATION NUMBER: PCT/US99/28564 FILING DATE: 1999-12-02
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Filvaroff, Ellen
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Botstein, David
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Hillan, Kenneth, J.
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Stewart, Timothy A.
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100.0%; Pred. No.
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5. 1.9e+02;
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; TYPE: PRT; ORGANISM: Homo Sapien US-09-906-838-236
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION E 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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CURRENT APPLICATION NUMBER: US/09/907.613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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LENGTH: 350
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Best Local Similarity 100.0%; Pred. No. 1.5
Matches 7; Conservative 0; Mismatches
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publication No. US20030027145A1
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APPLICANT: Ashkenazi, Avi
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Filvaroff, Ellen
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Grimaldi, Christopher J.
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Eaton, Dan L.
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Mather, Jennie P.
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Hillan, Kenneth, J.
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/3095
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-02
PRIOR PPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/30999
PRIOR APPLICATION NUMBER: PCT/US09/30999
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/907,942 CURRENT FILING DATE: 2002-01-22
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Publication No. US20030027146A1
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PRIOR APPLICATION NUMBER: PCT/US00/04414
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LENGTH: 350
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PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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Local Similarity 100.0%; F
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Eaton, Dan L.
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Botstein, David
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Best Local :
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SEQ ID NO 236
LENGTH: 350
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
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PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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             Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                            Fong, Sucre...
Gao, Wei-Qiang
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                                                                                Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                   Gerber, Hanspeter
Gerritsen, Mary E.
Pan, James
                                                                                                                        Goddard, A.
                                                                                                                                                                                                            Filvaroff, Ellen
                                                                                                                                                                                                                             Ferrara, Napoleone
                                                                                                                                                                                                                                                  Eaton, Dan L.
                                                                                                                                                                                                                                                                                   Botstein, David
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100.0%; Preu....
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100.0%; Pred. No.
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o. 1.9e+02;
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; ORGANISM: Homo Sapien US-09-904-820-236
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LENGTH: 350
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PRIOR FILING DATE: 2000-02-22
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                                                                                                                                                                                                                                         Sequence 236, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-13
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PRIOR APPLICATION NUMBER: PCT/US99/30095
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PRIOR FILING DATE: 1999-11-29
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APPLICANT: Genentech, Inc.
APPLICANT: Asikenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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RIOR APPLICATION NUMBER: PCT/US99/28564
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Stewart, Timothy A.
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Query Match
Best Local Similarity
The Tomac T; Conserva
                                                                                         US-09-904-859-236
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/65,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
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                                                                                                                                                SEQ ID NO 236
LENGTH: 350
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/30095
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                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER:
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                                                                                                                                TYPE: PRT
                                                                                                             ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US99/30999
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Filvaroff, Ellen
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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                  Conservative
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Result
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Listing first 100 summaries
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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203.827 Million cell updates/sec
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                                                                     OMPA_SERMA
TP50_TREPA
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OMPA_ESCFE
OMPA_ECOLI
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OM51_HAEIN
PORF_PSEFL
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PORF_PSEAE
OM53_HAEIN
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P07050 neisseria g
P02034 escherichia
P02934 scherichia
P02935 shigella dy
P03935 neisseria m
Q10557 mycobacteri
P24016 citrobacter
P02936 salmonella
P24754 escherichia
P34754 escherichia
Q99124 escherichia
Q99124 escherichia
Q99124 escherichia
Q99126 enterobacte
P24017 klebsiella
P57414 buchnera ap
Q93399 vibrio angu
P46233 vibrio para
P04845 serratia ma
P38369 treponema p
P286127 bacillus su
P24755 serratia od
                                                                                                                                                                                                                                                                                                                                                                                                     P38368
P13794
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P43840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                         4 escherichia
5 shigella dy
7 neisseria m
7 mycobacteri
6 citrobacter
6 salmonella
                                                                                                                                                                                                                                                                                                                                                           pseudomonas
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neisseria g
escherichia
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haemophilus
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pasteurella
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91 92 93 94 95 96 97 98 100	336 336 337 338 338 338 338 338 338 338 338 338	354
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09ji51 rattus norv 061702 mus musculu P27743 nocardia la P02982 escherichia P12881 drosophila 09z398 chlamydia p 057864 methanococc P95879 sulfolobus

l6 rattus norv 78 vibrio para

vibrio para 2 escherichia 1 tobacco rat

7 methanosarc 2 saccharomyc 3 mycobacteri 4 xylella fas methanosarc P22757 paracentrot Q29052 sus scrofa

streptomyce

halobacteri

5 drosophila 3 homo sapien 9 mesocricetu

mus musculu

P05649 bacillus su O51933 thermotoga

6 rhodospiril
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streptomyce helicobacte

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ALIGNMENTS

mycobacteri mycoplasma mesocricetu

salmonella corynebacte cyanophora pseudomonas

rhodobacter

P11031 Q9rvc3 Q22918 P02836 P06672 P53959

myxococcus
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> mycoplasma saccharomyc mycobacteri escherichia

neisseria g buchnera ap helianthus 2 salmonella 9 mycoplasma 8 escherichia

sparus aura semliki for

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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Peptidoglycan-associated lipoprotein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P43036
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PAL_ECOLI
P07176;
01-APR-1988
01-APR-1988
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 178:1699-1706(1996).
-i- FUNCTION: VERY STRONGLY ASSOCIATED WITH THE PEPTIDOGLYCAN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96198174; PubMed=8626299;
Rodriquez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.L.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAL OR PAL1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodom; PD000930; Bac_OmpA; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X74218; CAA52294.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro; IPR001145;
PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                 ERRAKAVORYLVLQGVSPAQLELVSYGEERPVATGNDEQSWAQNRRVEL
                                                                                                                                                                                                                                                                                            ERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL
                                                                                                                                                                                                                                                                                                                                                            -ALRAITTFYFEYDSSDLKPEAMRALDVHAKDLKANGN-RVVLEGNTDERGTREYNMALG
                                                                                                                                                                                                                                                                                                                                                                                                               LASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIAAAAAALSVLTFMTGCANKSTSQ----VMVAPNAPTGYTGVIYTGVAPLVDNDETVKA
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  (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Lipoprotein
  07, Created)
07, Last sequ
41, Last anno
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43.2%;
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     Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 316; DB 1;
Pred. No. 9.8e-22;
4; Mismatches 46
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PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN
N-ACYL DIGLYCERIDE (BY SIMILARITY).
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MEDLING 197061202; PubMed-8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizbuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lazzaroni J.-C., Portalier R.;
"The excC gene of Escherichia coli K-12 required for cell envelope integrity encodes the peptidoglycan-associated lipoprotein (PAL).";
Mol. Microbiol. 6:735-742(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the gene for the peptidoglycan-associated lipoprotein of Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87133578; PubMed=3545827;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli, and Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptidoglycan-associated lipoprotein precursor.
PAL OR EXCC OR B0741 OR Z0909 OR ECS0776.
                                                                                                                                                                                                                                                                                                    Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kikkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.,
                                                                   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe I ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.; Ruhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92244043; PubMed=1574003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yano M., Horluchi I.;
"A 718-kb DAR sequence of the Escherichia
corresponding to the 12.7-28.0 min region
DNA Res. 3:137-155(1996).
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=90078104; PubMed=2687247;
                   STRAIN=JM105
                                  SEQUENCE OF 1-30 FROM N.A.
                                                                                                                                                                                                                                                                           Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence of Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli K-12 genome on the linkage ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linkage map.";
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RESULT 3
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Best Local :
PAL_HAEIN STANDARD; PRT; 153 AA
P10324;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abergel C.; Walburger A., Chenivesse S., Lazdunski C.;
"Crystallization and preliminary crystallographic study of the
peptidoglycan-associated lipoprotein from Escherichia coli.";
Acta Crystallogr. D 57:317-319(2001).

-i- FUNCTION: Thought to play a role in bacterial envelope integrity.

Very strongly associated with the peptidoglycan.

-i- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; PD000930; Bac_OmpA; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoGene; EG10684; pal.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
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PIR; S20547; S20547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01021; OMPADOMAIN.
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67; Conserv
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                                                                                                                                                                                                                                                                                                       EYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY
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173 AA;
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Pred. No. 5.9
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      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute. There are no restrictions on its
                                                                                                                                          Outer membrane; Signal; Lipoprotein; Complete proteome
                                                                                                                                                                                                                                                                                                                  EMBL; M19391; AAA24994.1; -. EMBL; M18878; AAA24940.1; -. EMBL; U32722; AAC22039.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILINE=88115138; pubmed=2828309;
Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;
"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton protein from Haemophilus influenzae.";
                                                                     SEQUENCE
                                                                                      DOMAIN
                                                                                                                                     SIGNAL
                                                                                                                                                               PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_mpA; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                 Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                     TIGR; HI0381
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane protein P6 precursor (OMP P6) (15 kDa peptidoglycan-associated lipoprotein) (PC protein).
PAL OR OMPP6 OR HI0381.
                                                                                                                                                                                                                                                                                       PIR; A28543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=88085463; PubMed=3257200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and sequencing of Haemophilus influenzae outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 56:128-134(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                                                                                                                                                                                                                                                      A27558;
                    Similarity
                                                                                                                                                                                                                                                  IPR001145; Bac_OmpA
                                                                     153 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KW20
                                                                                                                                                                                                                                                                                     A28543
                                                                                                                                                                                                                                                                                                      A27558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170:489-498(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / ATCC 51907;
                                                                   16108 MW;
               30.7%;
   20;
                 Score 264; DB 1; Pred. No. 4.4e-17;
                                                                                   OMPA-LIKE
                                                                                                 OUTER MEMBRANE PROTEIN P6
N-ACYL DIGLYCERIDE.
                                                                   3DF358122EF17A11 CRC64;
   Mismatches
                               Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spotila L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by a lipid
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                                                                                                                                                                                                                                                                                                                                                                                                                  for
Gaps
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RESULT 4
PAL_PASMU
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                                          Matches
                                                       Query Match
Best Local
                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                        EMBL; U16849; AAA79373.1; --
EMBL; AE006136; AAK03050.1; --
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pasteurella multocida produces a protouter membrane protein of Haemophilus Infect. Immun. 63:989-993(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane protein P6 precursor (OMP P6) (P6-like) (Peptidoglycan-associated lipoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q51886;
                                                                                                                                              CHAIN
                                                                                                                                                            SIGNAL
                                                                                                                                                                          Outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                            May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of pasteurella multocida Pm70."; "Complete Acad. Sci. U.S.A. 98:3460-3465(2001).

-1- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Pm70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirsh D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95172751; PubMed-7868272; Kasten R.W., Hansen L.M., Hinojoza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAL OR PM0966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAL_PASMU
                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                             Pfam; PF00691; OmpA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21145866; PubMed=11248100;
                                                                                                                               LIPID
                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ANCHOR (By similarity).
SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                         membrane; Signal; Lipoprotein; Complete proteome.
L 1 19 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
             70
                                          50;
                                                         Similarity
                                                                                                                                                                                                                    PD000930;
                                                                                                                                                                                                                                 PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR
VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR
                                                                                                                                                                                      PS01068; OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
                                                                                             20
20
82
150
                                          Conservative
                                                                                                   ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                   Bac_OmpA; 1.
PROKAR_LIPOPROTEIN; 1
                                                                                                20
126
16213 MW;
                                                       30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Pasteurellaceae;
                                          19;
                                                       Score 258; DB 1;
Pred. No. 1.5e-16;
                                                                                                                            N-ACYL DIGLYCERIDE
                                                                                                                  OMPA-LIKE
                                                                                                                                             OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                   170E7B13D2E9ED6C CRC64;
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein with homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bieber D., Ruehl W.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                           34;
                                                                      Length 150
                                                                                                                              (BY SIMILARITY).
                                          Indels
                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seg
01-OCT-1994 (Rel. 30, Last ann
                                                                                                                                                                                                                                                                                                                                      Lipoprotein; Outer membrane; SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Legionella pneumophila.";
Infect. Immun. 59:2515-2521(1991).
-i- FUNCTION: VERY STRONGLY ASSOCIATED WITH THE PEPTIDOGLYCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ludwig B., Schmid A., Marre R., Hacker J.; "Cloning, genetic analysis, and nucleotide sequence of a determinant coding for a 19-kilodalton peptidoglycan-associated protein (Ppl) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=91310296; PubMed=1855972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AA100 / Serogroup 1;
MEDLINE=92114778; PubMed=1766377;
Engleberg N.C., Howe D.C., Rogers J.E., Arroyo J.,
"Characterization of a Legionella pneumophila gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAL OR PPLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptidoglycan-associated lipoprotein precursor
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01021; OMPADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X60543; CAA43033.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Legionella pneumophila
                                                                                                                                                                                                                                                                                  LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipoprotein antigen.";
Mol. Microbiol. 5:2021-2029(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legionellaceae; Legionella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A60337; A60337
S16631; S16631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
15 SAVLVAACSKTPGSA----DGGAAVGDGDATAQGLGQMTHFAGQEPGESYTTQAPHNQLYL 71
                                                       29 SQYMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL-----ASKLP----
                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYLSAKGVQAGQVSTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYFGFDKYNIEGEYVQILDAHAAFLNATPATKVVVEGNTDERGTPEYNIALGQRRADAVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PPL).
                                                                                                                                                                                                                             176
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                  22
22
                                                                                                                                                                                                                             ĀΑ;
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                                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                             18911 MW;
                                                                                                                                         28.5%;
36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Legionellaceae group;
                                                                                                              30;
                                                                                                                                         Score 245;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                            Antigen; Signal. POTENTIAL.
                                                                                                                                                                                                                                                          OMPA-LIKE
                                                                                                                                                                                                                                                                                  N-ACYL DIGLYCERIDE (PROBABLE)
                                                                                                                                                                                                                                                                                                               PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN.
                                                                                                                    Mismatches
                                                                                                                                                                                                                             7D9C3EBECBE621DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ormatics and the EMBL outstati
There are no restrictions on
ong as its content is in no
                                                                                                                                            DB 1;
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                                                                                                                                                                   Length 176;
                                                                                                                    Indels
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                                                                                                                    20;
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                                                             ----SLVY 71
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                                                                                                                    Gaps
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155 DPNRIYTEGKGKLNPIASNKTAEGRARNRRVEI 187

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RESULT ON THE PIT OF T
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Best Local
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Q05146;
Q1-OCT-1994 (Rel. 3
01-OCT-1994 (Rel. 3
01-FEB-1995 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.";
J. Bacteriol. 174:7729-7742(1992).
-!- FUNCTION: STRUCTURAL PROTEIN THAT MAY PROTECT THE INTEGRITY
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane protein from Bordetella avium and expression of the gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M96550; AAA22979.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane -!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93077456; PubMed-1447140;
Gentry-Weeks C.R., Hultsch A.-L., Kelly S.M., Keith J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BORAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequencing of a gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Curtiss R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella avium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
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138 NQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                        95
                                                                                                                                                             56
                                                                                                                                                                                             18 TFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 LLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                 47;
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                                                                                                                                                                                                                                                                                         Similarity
                                           TLKPEGRQLLDQVAQQARAIDLETIIAVGNTDSIGTEAYNMKLSERRAASVKAYLVSKGI 154
                                                                                            EIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGI
                                                                                                                                               TGIPGCDGVPVAQQPKEKPAPM------AAKVVFNADT------FFDFDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS01068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRMAGVSRQQIRVVSYGKERPANYGHDEASHAQNRRVEFIY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAYDDSTLASKYLPSVNAQAEYLKTHPGARVMIAGHTDERGSREYNVALGERRADTVAEI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDFDSDEIKFQAAAILDEQAQFLTINQTARVLVAGHTDERGSREYNMSLGERRAVAVRNY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   III;
                                                                                                                                                                                                                                                                                                                                                                     194 AA;
                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bac_OmpA; 1.
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30, Last sequence update)
31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  21115 MW;
                                                                                                                                                                                                                                                                                       21.5%;
30.7%;
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                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                 Score 185.5; DB ]
Pred. No. 7.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                           OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                            OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194
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                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
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OM51_HAEIN
                                                                                                                                                                                                                                                                                                 PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                Outer membrane; Transmembrane; Porin; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; HI1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Outer membrane protein P5 precursor (OMP P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMPA OR OMPP5 OR HI1164. Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001145; Bac_OmpA_
InterPro; IPR000498; OmpA_tmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P43840;
252 QATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS 311
                                                                                                                                                                                                                                                                                                                                                      PF01389; OmpA_membrane; 1
                                                                                                                                                                                                                                                                                                                                                                    PF00691; OmpA;
                            84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                          U32796; AAC22819.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         P02934; 1QJP.
                                                                                                                                     48;
                                                                                                                                                     Similarity
                                                                 PNTALNYNPWIGSINAGISYRFGQGAAPVVAAPEVVSKTFS-LNSDVTFAFGKANLKPQA
                                                                                              PNAPTGY----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                      353 AA;
                                                                                                                                                                                                                        326
272
                                                                                                                                   Conservative
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                                                                                                                                                                                                    37743 MW;
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                                                                                                                                                                                                                                                                                                                                                                                      OmpA_tmem.
                                                                                                                                27;
                                                                                                                                                 Score 176.5;
Pred. No. 9.8
                                                                                                                                                                                                                      OMPA-LIKE
                                                                                                                                                                                                                                  OUTER MEMBRANE
BY SIMILARITY.
                                                                                                                                                                                                                                                                     BY SIMILARITY
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                                                                                                                                   Mismatches
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144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171

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01-OCT-1994 (Rel. 3
01-OCT-1994 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG,
PSEUDOMONAS SPECIES OPRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPRF
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Mot R., Proost P., van Damme J., Vanderleyden J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas fluorescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF115334; AAD45981.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92167971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 25-74 AND 238-258
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                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 ATGYGKANPVTGATCDQVKGRKALIACFAPDRRVEIA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00691; OmpA;
279 QVLVKDGVAPSRITAVGYGESRPVADNATEAGRAVNRRVEAS 320
                                                                                                         219 VKFDFDKSVVKPNSYGDVKNLADFMAQYPATNVEVAGHTDSIGPDAYNQKLSQRRADRVK 278
                                                 130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F of P. aeruginosa and P. syringae.";
Jen. Genet. 231:489-493(1992).
                                                                                                                                                                70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR01021; OMPADOMAIN
                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                  Score 174; DB 1; Length 326, Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OUTER MEMBRANE PORIN F.
8 X 2 AA TANDEM REPEATS OF X-P
                                                                                                                                                                                                                                                                                                                                                                 OMPA-LIKE
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RESULT 9
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
Outer membrane protein P5 precursor (OMP P5
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P38368;
01-OCT-1994 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Munson R.S. Jr., Grass S., West R.;
"Molecular cloning and sequence of the gene for outer membrane
protein P5 of Haemophilus influenzae.";
Infect. Immun. 61:4017-4020(1993).
-i- SUBCELLULAR LOCATION: Integral membrane protein. Outer mem-
-i- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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STRAIN=1613 / Serot
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                                                                                                        144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171
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                                                             312 ATGYGKANPVTGATCDQVKGRKALIACLAPDRRVEIA 348
                                                                                                                                                252 QATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS
                                                                                                                                                                                           84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                             35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
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ID PORF_PSEAE STANDARD; PRT; 350 AA.
AC P13794;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

Outer membrane porin F precursor.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1. PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
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Pfam; PF00691; OmpA;
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MEDLINE-20437337; PubMed-
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ALSO HAS A STRUCTURAL ROLE IN DETERMINING CELL SHAPE AND ABILITY
TO GROW IN LOW-OSMOLARITY MEDIUM.
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
FYM: TWO DISULFIDE BONDS ARE PRESENT.
SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG, TO OTHER
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130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                      242 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR
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Pred. No. 2.7e-08;
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3 X 2 AA TANDEM REPEATS OF
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RESULT 12
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DOMAIN
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-!- FUNCTION: ACTS AS A FIMBRIAE SUBUNIT.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                      SEQUENCE
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Pfam; PF01389; OmpA_membrane; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94222575; PubMed=7909539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P45996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM53_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000930; Bac_On
PROSITE; PS01068; OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lim D., Demaria T., Bakaletz L.;
"Role of fimbriae expressed by nontypeable Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001145; Bac_OmpA
                                                                                                                                                                                 199
                                                            318 ATGYGEANPVTGATCDQVKGRKALIACLAPDRRVEIA 354
                                                                                                                                                 84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
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5
                                                                                          IISFGEERPIAFGTNEE---
                                                                                                                      QATILDSVYGEISQVKSRKVAVAGYTNRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pean Bioinformatics Institute. The non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                 PNTAINYNPWIGCINAGISYRFGQGEAPVVAAPEMVSKTFS-LNSDVTFAFGKANLKPQA
                                                                                                                                                                                                            PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA
                                                                                                                                                                                                                                                                                                      359 AA;
                                                                                                                                                                                                                                                                                                                     332
278
                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                     359
344
322
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29.9%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                 FALSE_NEG
                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                        Score 165.5; DB Pred. No. 9.9e-08
                                                                                                                                                                                                                                                                                                                                 OUTER MEMBRANE PROTEIN P5
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                      OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                      576B1C59B4818C37 CRC64;
                                                                                                                                                                                                                                          Mismatches
                                                                                        -AWSQNRRAELS
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                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                        Length 359;
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                                                                                                                                                                                                  RESULT 13
YIAD_ECOLI
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                                                                                                                       YIAD_ECOLI
P37665;
01-OCT-1994
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P22263;
01-AUG-1991 (Rel.
01-AUG-1991 (Rel.
15-JUL-1999 (Rel.
               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Hypothetical lipoprotein yiaD precursor.
YIAD OR B3552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformaticy Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000930; Bac_OmpA; 1. prostTF: PS01068: OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane; Transmembrane; Porin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M55408; AAA25910.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ullstrom C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91100367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC 19310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas syringae (pv. syringae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane porin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conservation of the gene for outer membrane protein OprF in t
family Pseudomonadaceae: sequence of the Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Conservation of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hancock R.E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein PTM: TWO DISULFIDE BONDS ARE PRESENT. SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: HAS PORIN ACTIVITY, FOR ALSO HAS A STRUCTURAL ROLE IN DET TO GROW IN LOW-OSMOLARITY MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSEUDOMONAS SPECIES OPRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A39139; A39139
                                                                                                                                                                                                                                                                                                 296 QVLVNQYGVGASRVNSVGYGESKPVADNATEAGRAVNRRVE
                                                                                                                                                                                                                                                                                                                                                                                                      236
                                                                                                                                                                                                                                                                                                                                                130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR01021; OMPADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR
                                                                                                                                                                                                                                                                                                                                                                                                 VKFDFDKSVVKPNSYGDIKNLADFMQQYPQTTTTVEGHTDSVGPDAYNQKLSERRANAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .A., Siehnel
coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                        STANDARD;
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19,
38,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36567 MW;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woodruff W., Steinbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 163.5; DB 1
Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
OUTER MEMBRANE PORIN
                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5B463D9AD973D755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IY, FORMING SMALL WATER-FILLED IN DETERMINING CELL SHAPE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                            LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and nucleotide sequence of bisC, the structural gene for biotin sulfoxide reductase in Escherichia coli.";
J. Bacteriol. 172:2194-2198(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sofia H.J., Burland V., Daniels D.L., Plur "Analysis of the Escherichia color genome. region from 76.0 to 81.5 minutes.", Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000432; AAC76576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U00039; AAB18529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CAUTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pierson D.E., Campbell A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01068; OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90202748; PubMed=2180922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-104 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Attached to the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMESHIFT IN POSITION 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Probable)
                                                                                                    211
                                                                                                                             167
                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR001145; PF00691; OmpA;
                                                                                                                                                                                        107
                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                            47 TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG 106
                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                       HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR
                                                                                                                               RAELS
                                                                                                                                                           YTDSTGGHDLNMRLSQQRADSVASALITQGVDASRIRTQGLGPANPIASNSTAEGKAQNR
                                                                                                                                                                                                                   TGVSVTRSGDNII-----LNMPNNVTFDSSSATLKPAGANTLTGVAMVLKEYPKTAVNVIG
                                                                                                    RVEIT
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                                                                                                                                                                                                                                                                                                                                                           20
219
21
                                                                                                                                                                                                                                                                                                                                22169 MW;
                                                                                                                                                                                                                                                                                       17.9%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bac_OmpA.
                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                       Score 154; DB 1
Pred. No. 6e-07;
                                                                                                                                                                                                                                                                                                                                                OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL LIPOPROTEIN YIAD.
N-ACYL DIGLYCERIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                8EDED55A0A66E368 CRC64;
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plunkett G. III, Blattner F.R.; ome. V. DNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as its content
                                                                                                                                                                                                                                                                                                    ۳.
                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                    Length 219;
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                           210
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OMP3_NEIGO STANDARD; P07050; 01-APR-1988 (Rel. 07, Created)

236

B

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OMPA_ESCFE
ID OMPA_E
AC P24747
DT 01-MAR
DT 01-MAR
DT 01-NOV
DE Outer
GN OMPA.
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                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 35
                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Outer membrane protein A (Outer membrane prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The DNA sequence of the structural gene of gonococcal protein III and the flanking region containing a repetitive sequence. Homology protein III with enterobacterial OmpA proteins.";

J. Exp. Med. 165:471-482(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87139801; PubMed=3: Gotschlich E.C., Seiff M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1988 (Rel. 07, 01-FEB-1994 (Rel. 28,
                                                                                                                                                    OMPA_ESCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X05105; CAA28752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000930; Bac_Ompa; 1. PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01021; OMPADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PIII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produ-
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SÜBCELLULAR IOCATION: Intégral membrane protein. Outer membrane MISCELLANEOUS: PIII IS CLOSELY ASSOCIATED WITH PART, BUT NOT AL OF THE PI MOLECULES IN THE GONOCOCCAL OUTER MEMBRANE.

MISCELLANEOUS: A PORTION OF THE PIII IS EXPOSED TO THE SURFACE INTACT GONOCOCCI; THE PROTEIN CAN BE LABELED WITH IODINE AND REACTS WITH MABS.

SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG, TO N.MENINGITID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A27894; A27894.
rPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                143 YNQALSERRAYVVANNLVSNGVPASRISAVGLGESQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00691; OmpA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                             YNMSLGERRAVAVRNYLLGKGINQASVEIISFGEER 151
                                                                                                                                                                                                                                                                                                                                                                                DETISLSAKTL-----FGFDKDSLRAEAQDNLKVLAQRLSRTNVQSVRVEGHTDFMGSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                  DETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSRE
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23
69
69
71
73
73
131
131
185
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                       protein A (Outer membrane protein II) (Fragment)
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                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3102671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.6%;
36.5%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Antigen; Signal; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.III precursor (Gonococcal protein III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blake M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 151.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OUTER MEMBRANE PROTEIN P.II
4 X 2 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAE9AAECA66FB199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1e-06;
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                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO N.MÉNINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane.
ART, BUT NOT ALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL
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                     Qy
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                                                                                                                                                     Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular and evolutionary relationships among enteric bacteria.";
J. Gen. Microbiol. 137:1911-1921(1991).
-!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR T
                                                                                                                                                                                                                   VARIANT
NON_TER
                                                                                                                                                                                                                                             DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 35471, ATCC 35469, a MEDLINE=92065252; PubMed=1955870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=564;
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia fergusonii.
                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001145; InterPro; IPR000498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence J.G., Ochman H., Hartl D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOLUTES (BY SIMILARITY).
SUBUNIT: MONOMER (PROBABLE).
SUBURITAR LOCATION: Integral membrane protein. Oute
SUBCELLULAR LOCATION: Integral membrane protein. Oute
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AN RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                  166
                        160
                                                                           107
                                                                                                     106
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00691; OmpA; 1. PF01389; OmpA_membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M63352; AAA24236.1; -. M63351; AAA24232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M63353; AAA24240.1; P02934; 1QJP.
                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                 PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCC 35472
                                                                                                                                                                    Similarity
LIDCLAPDRRVEI 238
                                                  YTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTCDNVKQRAA
                                                                                                   VAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSNLDPKDGSVVVLG
                       --EAWSQNRRAEL 170
                                                                           HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE------
                                                                                                                            VAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAG
                                                                                                                                                                                                          243 AA;
                                                                                                                                                                                                                                                                                                                          48
65
87
107
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Phage recognition; Repeat; Porin.
                                                                                                                                                                                                                                                                                                8
27
59
81
98
114
108
110
                                                                                                                                                                17.2%;
31.6%;
                                                                                                                                                                                                          26144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bac_OmpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OmpA_tmem.
                                                                                                                                                                                                          WW;
                                                                                                                                                      20;
                                                                                                                                                                  Score 148.5;
Pred. No. 2.1
                                                                                                                                                                                                                           OMPA-LIKE.
BY SIMILARITY.
E -> D (IN STRAIN ATCC 35469).
                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                                                                          B89F7FC29D42E3AB CRC64;
                                                                                                                                                                                                                                                                                                                            X 2 AA TANDEM REPEATS OF A-P.
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCC
                                                                                                                                                                  2.1e-06;
                                                                                                                                                                                DB 1;
                                                                                                                                                      60;
                                                                                                                                                      Indels
                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane
AINS ATCC 35471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL
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STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M.,
Han C.-G., Ohtsubo E., Nakayama K.,
                                                                                                                                                                                                                             Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K. Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage mathematical DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Movva N.R., Nakamura K., Inouye M.;
"Gene structure of the OmpA protein, a major surface protein
"Secherichia coli required for cell-cell interaction.";
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                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-K12 / MG1655;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                              Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97061202; PubMed=8905232;
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21-JUL-1986
                                                                                                                      SEQUENCE FROM
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A
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  Murata
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  Tanaka
                          Ishii
                                                                                                                                                                                                     coli 0157:H7.";
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  Yokoyama
Tobe T.,
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Gromiha M.M., Ponnuswamy P.k.;
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                                          MEDLINE=99296577;
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                                                                       TOPOLOGY
                                                                                                                                                     MEDLINE=94148615;
                                                                                                                                                                   TOPOLOGY
                                                                                                                                                                                                                    Sugawara E., Nikaido H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          separation using two-dimensional gel electrophoresis."; Electrophoresis 19:837-844(1998).
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STRAIN=K12 / W3110;
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in the genome of Escherichia coli K-12.";
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Pasquali C., Sanchez J.-C., Ravier F.,
Frutiger S., Paquet N., Wilkins M., App
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81054820; PubMed=7001461;
                                                                                                                                                                                                         "Pore-forming activity
                                                                                                                                                                                                                                                             PORIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                            MEDLINE=86033606;
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                                                                                                                                                                                                                                    MEDLINE=92129334;
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181:3688-3694(1999).
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                                                                                                                                                                                                                                                                                                                                                                                  159:570-578(1984).
                                                                                                                                                                                        activity of OmpA protein of Escherichia coli."; 267:2507-2511(1992).
                                                        PubMed=10368142;
                                                                                                                                                                                                                                                                                                                                                        TO PHAGE ENTRY.
                                                                                                                                                  PubMed=8106193;
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                                                                                                                                                                                                                                                                                                                                          PubMed=3902787;
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                                                                                                                                                                                                                                                                                                                membrane protein OmpA of
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H.;
                                                                                                                          hydrophobic
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II (ompA protein)
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Matches
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SWISS-2DPAGE; P02934; COLI.

ECO2DBASE; F024.5; 6TH EDITION.

ECO2DBASE; F028.0; 6TH EDITION.

ECO2DBASE; F033.0; 6TH EDITION.

ECO2DBASE; F033.1; 6TH EDITION.

ECOGENE: EG11069; ompA.

InterPro; IPR001145; Bac_OmpA.

InterPro; IPR00149; ompA. tmem.
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Pfam; PF01389; OmpA_membrane; 1.
Pfam; PF01389; OmpADOMAIN.
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EMBL; D90733; BAA35715.1; --
EMBL; D90734; BAA35722.1; --
EMBL; AE005286; AAG55443.1; --
EMBL; AE002554; BAB34464.1; --
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-I- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE ACTION OF COLUMN RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
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PDB; 18XW; 30-DEC-98.
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Nat. Struct. Biol. 5:1013-1017(1998).
[17]
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X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e Coutre J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
MASS SPECTROMETRY: MM-35177; METHOD-Electrospray; RANGE-22-346.
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                                                                                                                                                                                       VAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSNLDPKDGSVVVLG
                                     --EAWSQNRRAEL 170
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31.6%;
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                                                                                                                                                                                                                                                                                            Score 148.5; DB 1;
Pred. No. 3.2e-06;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                            Length 346;
                                                                                                                                                                                                                                                                                              Indels
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OR RESULT
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Query Match
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P02935;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
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Nucleic Acids Res. 10:2367-2378(1982).

-i- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
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_SHIDY
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REPEAT
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REPEAT
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InterPro; IPR001145; Bac_OmpA.
InterPro; IPR000498; OmpA_tmem.
Pfam; PF00691; OmpA; 1.
Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMMBL outstart the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa; 1. PROSITE; PS01068; OMPA; 1.
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Braun G., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
                                                                                 SEQUENCE
                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; V01344; CAA24638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOLUTES (BY SIMILARITY).
SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 LIDCLAPDRRVEI 332
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17.2%;
31.6%;
                                                                           MW;
                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
Score 148.5; DB 1; Pred. No. 3.3e-06;
                                                                                                      OMPA-LIKE.
BY SIMILARITY.
                                                                                                                                                                                                                                                        POTENTIAL.
4 X 2 AA TANDEM REPEATS OF A-P
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                                                                                                                                                                         Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E. Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Haft D.H., Clack A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Sequence of the structural gene (rmpM) for the class 4 outer membrane protein of Neisseria meningitidis, homology of the protein to gonococcal protein III and Escherichia coli OmpA, and construction of meningococcal strains that lack class 4 protein. "; Infect. Immun. 57:2066-2071(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMP4_NEIMA
P38367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _NEIMA
                                                                                             MC58.";
Science 287:1809-1815(2000).
Integral membrane
                                                                                                                                                                                                                                                                                                                     WEDLINE=20175755; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CCUG 18241 / M986 / Serogroup B / SMEDLINE=89277523; PubMed=2499543; Klugman K.P., Gotschlich E.C., Blake M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup A), Neisseria meningitidis (serogroup B).
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                   between
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                                                                                                                                                                                                                                                                                                                                                                                                       Nature
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MEDLINE=20222556; PubMed=10761919;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                               "Complete genome sequence of Neisseria meningitidis serogroup B
European
                                                                                         SIMILARITY: BELONGS
               SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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Best Local
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01-OCT-1996
01-OCT-1996
15-JUN-2002
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                                                                                                                                                                                                     STRAIN-H37Rv;
                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       NCBI_TaxID=1773;
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Pfam; PF00691; OmpA;
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242 AA;
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MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Berliwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Rv0899.
RV0899 OR MT0922 OR MTCY31.27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 YNQALSERRAYVVANNLVSNGVPVSRISAVGLGESQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 YNMSLGERRAVAVRNYLLGKGINQASVEIISFGEER 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 DETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSRE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DETISLSAKTL----FGFDKDSLRAEAQDNLKVLAQRLGQTNIQSVRVEGHTDFMGSDK
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BY SIMILARITY.
MISSING (IN ST
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Pred. No. 4.9
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I -> V (IN STRAIN MC58).
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Best Local
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P24016;
01-MAR-1992 (Rel. 2
01-MAR-1992 (Rel. 2
01-NOV-1995 (Rel. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                              01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Outer membrane protein A (Outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; FALSE_NEG.
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  SEQUENCE FROM N.A. STRAIN=OS60;
                                                                                    Citrobacter
                                                                                                      Bacteria; Proteobacteria;
                                                                                                                           Citrobacter freundii
                                                                                                                                               OMPA.
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                                                            NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                           281 VADYLVARGVAGDHIATVGLGSVNPIASNATPEGRAKNRRVEI 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 TLTGTAPSSEHKDAVKRAATSTWPDMKIVNNIEVTGQAPPGPPASGPCADLQSAINAVTG
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326 AA;
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    typhimurium
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Lawrence J.G., Ochman H., Hartl D.L.;

"Molecular and evolutionary relationships among enteric bacteria.";

J. Gen. Microbiol. 137:1911-1921(1991).

-i- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
OMPA_SALTY STANDARD; PRT; 350 AA.

P02936;
21-JUL-1986 (Rel. 01, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Outer membrane protein A precursor (Outer membrane protein 33K) (Outer membrane major heat-modifiable protein).
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Pfam; PF01389; OmpA_membrane; 1.
ProDom; PD000930; Bac_OmpA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M63354; AAA23095.1; -. HSSP; P02934; 1QJP.
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InterPro; IPRO00498;
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SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane SIMILARITY: BELONGS TO THE OMPA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
                                                                                                                                                                                                                                                                                                                                           148 GEERPIAFGTNE-----EAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                          202 GESNPVTGNTCDNVKARAALIDCLAPDRRVEI 233
                                                                                                                                                                                                                                                                                                                                                                                              142 MYSQLSNLDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GLLSVGVSYRFGQQEEAAPVVVAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQQALDQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 GVIYTGV-----APLVDNDETVKALASK---LPSLVYFDFDSDEIKPQAAAILDE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                            90 QAQELTT--NQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISF 147
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Pred. No. 9.9e-06;
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InterPro; IPR001145; Bac_OmpA.
InterPro; IPR000498; OmpA_tmem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
          SEQUENCE
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Pfam; PF01389; OmpA_membrane; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spiet
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MEDLINE=83287368; PubMed=6349993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Complete genome sequence of Salmonella enterica serovar Typhimurium
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SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
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Best Local Similarity
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EMBL; M63347; AAA24238.1;
HSSP; P02934; 1BXW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawrence J.G., Ochman H., Hartl D.L.; "Molecular and evolutionary relationships among enteric bacteria."; J. Gen. Microbiol. 137:1911-1921(1991).
                                                                                                                                                                                                                                  Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBUNIT: MONOMER (PROBA
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SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
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bred. No. 1.7e-05;
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Q99124; Q03617;
01-NOV-1997 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawrence J.G., Ochman H., Hartl D.L.;
"Molecular and evolutionary relationships among enteric bacteria.";
J. Gen. Microbiol. 137:1911-1921(1991).
-!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND I. AND FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                     InterPro; IPRO01145; Bac_OmpA.
InterPro; IPRO00498; OmpA_tnem.
Pfam; PF00691; OmpA_ 1.
Pfam; PF01389; OmpA_membrane; 1.
ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 33429; ATCC 29907, and ATCC 33430;
MEDLINE-92065252; PubMed-1955870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
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                                                                                                                                                                                                     EMBL; M63343; AAA24235.1; -.
EMBL; M63344; AAA24239.1; -.
EMBL; M63345; AAA24242.1; -.
HSSP; P02934; 1QJP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
Outer membrane; Transmembrane; Phage recognition; Repeat; Porin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOLUTES (BY SIMILARITY).
SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATCC 33429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 LIDCLAPDRRVEI 238
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AAA24239.1; -.
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4.
OMPA-LIKE.
BY SIMILARITY.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                           membrane protein OmpA from Enterobacter aerogenes.";
Eur. J. Biochem. 137:495-500(1983).
-i- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHACES. ALSO ACTS AS A PORIN WITH LOW DERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                Outer membrane protein A precursor
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                    Braun G., Cole S.T.;
                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=84108348; PubMed=6363059;
                                                                                                                                                                                                                                                  NCBI_TaxID=548;
                                                                                                                                                                                                                                                                Enterobacter
                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                        Enterobacter aerogenes (Aerobacter aerogenes).
                                                                                                                                                                                       "Molecular characterization of the gene coding
                                                             SOLUTES (BY SIMILARITY).
SUBBURIT: MONOMER (PROBABLE).
SUBCELLULAR LOCAFION: Integral membrane protein. Outer membrane.
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 GEERPIAFGINE-----EAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 LYTQLSNLDPKDGAVVVLGYTDRIGSDAYNQRLSQQRAQSVVDYLVSKGIPAGKITAQGQ
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241 AA;
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25986 MW;
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27.0%; Pred.
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V -> G (IN STRAIN ATCC 29907).

W -> M (IN STRAIN ATCC 33430).

MISSING (IN STRAIN ATCC 33430).

N -> S (IN STRAIN ATCC 29907 AND STRAIN ATCC 33430).

K -> Q (IN STRAIN ATCC 29907 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
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Pred. No. 1
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 Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A., Baussant T., Haeuw J.F., Uhlen M., Binz H., Stahl S.; "Chromosomal sequencing using a PCR-based biotin-capture method allowed isolation of the complete gene for the outer membrane pro
                                                                                                                                                               OMPA_KLEPN STANDARD; PRT; 344 AA. P24017; 069435; 01-MAR-1992 (Rel. 21, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                 MEDLINE=98192544; PubMed=9524233;
                                                              STRAIN=RV 308;
                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                   Klebsiella pneumoniae
                                                                                                                                                        Outer membrane protein A precursor
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SEQUENCE
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                                                                        SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=573;
                                                                                                              Klebsiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000930;
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Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S07222; S07222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                   154 AFGT 157
                                                                                                                                                                                                                                                                            311 TGNT 314
                                                                                                                                                                                                                                                                                                                                         96 T--NQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPI 153
                                                                                                                                                                                                                                                                                                                                                                                       36 NAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P02934; 1QJP
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                     NMDPKDGSAVVLGYTDRIGSEQYNQKLSEKRAQSVVDYLVAKGIPANKISARGMGESDPV
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315
350
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                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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Pred. No. 3.2e-05;
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the outer membrane protein
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Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular and evolutionary relationships among enteric bacteria.";
J. Gen. Microbiol. 137:1911-1921(1991).
-!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A of Klebsiella pneumoniae.";
Gene 210:93-101(1998).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M63355; AAA25119.1;
HSSP; P02934; 10JP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01068; OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001145; Bac_OmpA
InterPro; IPR000498; OmpA_tmer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                               Local
                                                          124
                                                                                                          215
                                                                                                                                                66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER
                                                                                                                                                                                                                               Similarity
RAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330
                                                  RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE----
                                                                                                  LKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEK
                                                                                                                                                                                                                                                                                                      344 AA;
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                      37061 MW;
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Y -> I (IN REF
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4 X 2 AA TANDEM REPEATS
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                                                                                                                                                                                                     Mismatches
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RESULT 26

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RESULT 27
MOTY_VIBAN
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Best Local
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Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P57414;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR001145; Bac_OmpA.
InterPro: IPR000498; OmpA_tmem.
Pfam; PF00691; OmpA; 1.
Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OmpA-like protein precursor. OMPA OR BU332.
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20445173; PubMed=10993077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
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                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MONOMER (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL SOLUTES (BY SIMILARITY).
                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P02934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP001119; BAB13037.1; -.
                                                                                                                                             34;
                                                                                                                                                         Similarity
                                                                     RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE 159
                                                                                                                  DNDETVKALASKLPSLVYFDFDSDEIKPQA---AAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                                             DDSEPLNEQYSVLNENINFPFNSTELKPSSYDKLNKLDDDIKDMQLKNVSIVLL-GHADK
                                               IGSDEYNQKLSEDRAYSIKNYLASRGFSRDKITVKGMGKLYPL---TNQ 319
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31.2%;
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                                                                                                                                                       Score 135.5;
Pred. No. 4.9
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                                                                                                                                                                                                                                                                                                                                      OMPA-LIKE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
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                                                                                                                                                                                          CC14AB1BD590CF58 CRC64;
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 AA.
                                                                                                                                                    4.9e-05;
                                                                                                                                                                 DB 1;
                                                                                                                                            45;
                                                                                                                                                                 Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishikawa H.;
                                                                                                                                            Indels
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                                                                                                                                           7;
                                                                                                                                         Gaps
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Db
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                                                                                                                                                                                                                                                                             MOTY_VIBPA
                                                                                                                                                                                                                                                                                                       RESULT 28
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                              01-NOV-1995
01-NOV-1995
01-FEB-1996
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOTY_VIBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uncontrol by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for common entities remarkes a light and the statement of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The role of motility in adherence and invasion of a fish cell line by Vibrio anguillarum.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS THE ROLE OF A STATOR IN THE SODIUM FLAGELLAR MOTOR, STABILIZING THE FORCE-GENERATING UNIT THROUGH DIRECT INTERACTION WITH THE CELL WALL. INVOLVED IN ADHERENCE AND INVASION OF FISH CELL LINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-NB10 / Serotype 01;
Ormande P., Milton D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium-type flagellar protein moty precursor (Polar flagellum motor
                                            Vibrio parahaemolyticus.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                           MOTY_VIBPA
P46233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio anguillarum (Listonella anguillarum).
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                         Sodium-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flagella; Signal.
SIGNAL 1
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InterPro; IPR001035; MotY.
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                       NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01068; OMPA; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF176946; AAD51752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                              243 VLRDYFKSLGLPEDRIQVQGYGKRRPIADNASPIGKDKNRRVVIS
                                                                                                                                                                                                                                                                                                                                                                                                                           127 AVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR01023; NAFLGMOTY. PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILHYDRDNVQLNKASQKRLAQIADYIRYNQDIDLVLVSTYTDSVDSRGVSQDLSERRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTA-RVLVAGHTDERGSREYNMSLGERRAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220
293 AA;
                                                                                                                    (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 33, Last annotation updat
flagellar protein MOTY precurso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                     STANDARD;
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293
264
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28.6%;
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                                               gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 127.5; DB 1
Pred. No. 0.00021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMPA-LIKE.
; 5618435B49F40D3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SODIUM-TYPE FLAGELLAR PROTEIN MOTY.
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                                                                                                                                                                                                                                                     PRT;
                                                                                                                      ion update) precursor.
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CCCCCCRTTTAX
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OMPA_SE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein A precursor.
                                                                                                                                                                                                                                                                                                                                                                                   P04845;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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-!- FUNCTION: PLAYS THE ROLE OF A STATOR IN THE SODIUM FLAGELLAR MOTOR, STABILIZING THE FORCE-GENERATING UNIT THROUGH DIRECT
                                                                                                                membrane protein.";
Mol. Gen. Genet. 195:321-328(1984).
                                                                                                                                                  "DNA sequence analysis of the Serratia marcescens ompA gene: implications for the organisation of an enterobacterial outer
                                                                                                                                                                                              Braun G., Cole S.T.;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=85035845; PubMed=6092858;
                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                 Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMPA_SERMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001035; Moty.
                                                                                                                                                                                                                                                                       NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                           Serratia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flagella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94292449; PubMed=8021208;
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WITH LOW
SOLUTES (
SUBUNIT:
                                    FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH THE CELL WALL.
SUBCELLULAR LOCATION: Membrane-associated (Potential).
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 TILHYEROGDQLTKASKKRLAQIADYVRHNQDIDLVLVATYTDSTDGKSESQSLSERRAE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 SLRTYFESLGLPEDRIQVQGYGKRRPIADNGTPIGKDKNRRVVIS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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293 AA;
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                    (BY SIMILARITY)
    MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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293
264
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  (PROBABLE).
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                                                                                                                                                                                                                                                                                                           gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
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Pred. No. 0.
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SODIUM-TYPE FLAGELLAR PROTEIN MOTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                   update)
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AC DT DT DT DT OS OS RN RN RN RA
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Best Local S
Matches 34
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TP50_TREPA STANDARD;
p38369; Q56358;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last seq
16-0CT-2001 (Rel. 40, Last anno
MEDLINE=94156449; PubMed=8112835; Hardham J.M., Stamm L.V.;
                                                                                                                                                                                                             Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                 01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein TPN50 precursor (Antigen TPP57).
                                                                             STRAIN=Nichols;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  TPN50 OR TP0292
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                                                                                                                                                                                  NCBI_TaxID=160;
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Pfam; PF01389; OmpA_membrane; 1.
PRINTS; PR01021; OMPADOMAIN.
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InterPro; IPR001145; Bac_OmpA.
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Pred. No. 0.00084;
9; Mismatches 49
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RESULT 31
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                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ptam; PF00691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities recurred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Nichols;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and characterization of the Treponema pallidum tpn50 gene, an ompA homolog.";
                                                                                                                                                                                                                                                 Local
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                               371 RYLQELGVVDAAHVYTRGCGAQQSIAPNDSEDGRRKNRRVEIT 413
                                                             130 NYLLGKG-INQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                         311 VQFDADSASLAPSEYEKLRKIAELLRAFPDRELLVSGHAARRGSVQDQQRISEERADVVA
                                                                                                                                                     253 SGGTVLRYQGTATAKNFAPERFDPARTVVELQETLKDL--HMPDAKVRETEEGVTISIEN 310
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                                                                                                                       70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREVNMSLGERRAVAVR 129
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417 AA;
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417
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127
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27.0%;
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A -> E (IN REF. 2).
; 079F579CFDD7288C CRC64;
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                                                                                                                                                                                                                          Mismatches
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RA Chois.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Epilita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA JOris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Medina N., Mellado R., Liu H., Masuda S., Mauel C., Medigue C.,
RA Konone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parsocan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Tamakoshi A., Tanaka T., Tarahahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Wipat A., Yandenbol M., Vannier F., Vasarotti A.,
RA Winters P., Wipat A., Yandamoto H., Yannier F., Vasarotti A.,
RA Winters P., Wipat A., Yandamoto H., Yannier F., Vasarotti A.,
RA Winters P., Wipat A., Yandamoto H., Yannier F., Vasarotti A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA Yoshida K., Yoshikawa H.F., Zumstein
PIR; B42882; B42882.
SubtiList; BG10689; motB.
InterPro; IPR001145; Bac_OmpA
                                                                                             EMBL; M77238; AAA22603.1; -.
                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
-!- FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR. MIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier I., Brans A., Brann M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mirel D.B., Lustre V.M., Chamberlin M.J.;
"An operon of Bacillus subtilis motility genes transcribed by the sigma D form of RNA polymerase.";
J. Bacteriol. 174:4197-4204(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92325000; PubMed=1624413;
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                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type II membrane protein. SIMILARITY: BELONGS TO THE MOTB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                     CELL WALL
                                                                                                                                                                                                                                                                                                                                                                                                                          BE A LINKER THAT FASTENS THE TORQUE-GENERATING MACHINERY
                                                                    S27516; S2751
                                                                                                                                                                                           non-profit institutions as long as its content and this statement is not removed. Usage hy and requires a license armon-
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMPA_SEROD STANDARD; PRT; 243 AA. P24755; 01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 01-Mar-nembrane protein A (Outer membrane protein II) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serratia odorifera
                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   LAWRENCE J.G., Ochman H., Hartl D.L.;

"Molecular and evolutionary relationships among enteric bacteria.";

"Molecular and evolutionary relationships among enteric bacteria.";

J. Gen. Microbiol. 137:1911-1921(1991)

J. Gen. Microbiol. 137:1911-1921(1991)

FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92065252; PubMed=1955870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=ATCC 3307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=618;
                          InterPro; IPR001145; Bac_OmpA.
InterPro; IPR000498; OmpA_tmem
                                                                                                                                                                     the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                 EMBL; M63357; AAA26561.1; -.
                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane. SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                     SOLUTES (BY SIMILARITY).
SUBUNIT: MONOMER (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 RAVAVRNYLLGKGINQASV-EIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 SLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD----ERGSREYNMSLGER 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 IVLYASSSIDAAKFQML-----SKSFNEVF-----TGGTGVLDYSSVTPPENESDGI 80
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PF00691; OmpA; 1
PF01389; OmpA_mer
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42
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OmpA_membrane; 1.
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                               OmpA_tmem.
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RESULT 33
YTXE_BACME
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01-NOV-1995
01-NOV-1995
16-OCT-2001
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prosite; PS01068; OMPA; FALSE_NEG
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                                                                                                                                                                                                                                                       Hueck C., Kraus A., Hillen W.;
"Sequences of copA and two downstream Bacillus megaterium genes with homology to the motAB operon from Bacillus subtilis.";
Gene 143:147-148(1994).
Gene 143:147-148(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                       Bacillus megaterium.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
                                                                                                                          modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                     MEDLINE=94259294; PubMed=8200532;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTXE_BACME
                                               ProDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Transport; Transmembrane
                                                                Pfam; PF00691; OmpA; 1.
ProDom; PD000930; Bac_O
                                                                                          InterPro;
                                                                                                   EMBL; L26052; AAA22297.1; -
                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MOTB FAMILY.
                            TRANSMEM
                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 LKSDYLFNSAKSSLKPEGQQALDQLYTQLSSMDPKDGSYVYLGYTDPVGKDAANQKLSEA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 RARSVVDYLVSKGIPADKISARGMGEADQVTDSCGYKNGRATKAQIECLAPNRRVEI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 RAVAVRNYLLGKGINQASVEIISFGEERPI-----AFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER 123
                                                                                        IPR001145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 AA;
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
1 24.6 kDa protein in CCPA 3'region (ORF2).
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29.1%;
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                                                                                          Bac_OmpA.
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Pred. No. 0.022;
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EXTRACELLULAR (POTENTIAL).
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SEQUENCE DOMAIN

218 AA; 36

24642 MW;

63622D730A4AE247 CRC64;

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RESULT 34
YFIB_ECOLI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wimpodified and this statement is not removed. Usage by and for commercia
                                                                                                                     MEDLINE=83141045; PubMed=6298574;
Bystroem A.S., Bjoerk G.R.;
"The structural gene (trmD) for the tRNA(mlG)methyltransferase is part of a four polypeptide operon in Escherichia coli K-12.";
MOL. Gen. Genet. 188:447-454(1982).
-i- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                               Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampel G., Satoh Y., Sivasundaram S. Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.
                                                                                                                                                                                                                                                                                      analysis of its sequence features.";
                                                                                                                                                                                                                                  SHOWS THAT THE PROTEIN IS EXPRESSED
                                                                                                                                                                                                                                                                                              "Construction of a contiguous 874-kb sequence of the Escherichia coli-
K12 genome corresponding to 50.0-68.8 min on the linkage map and
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97349980; PubMed=9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bystroem A.S., Hjalmarsson K.J., Wikstroem P.M., Bjoerk G.R.;
"The nucleotide sequence of an Escherichia coli operon containing genes for the tRNA(mlo)methyltransferase, the ribosomal proteins and L19 and a 21-K polypeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1988 (Rel.
01-AUG-1992 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                         ramagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=84057772; PubMed=6357787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative lipoprotein yfiB precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFIB OR B2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                      Res. 4:91-113(1997).
                                                                                                                  (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AARASGVIRYLTNHFSLSANRFEALGYGDTKPLVPNTSNDNLQKNRRVEI 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 LQEQVLFETGQADILKKGTPFLDELGRLFSTIPN-DIKVEGHTDNRPIHTYAYPSNWELS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY----NMSLG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERRAVAVRNYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07, Created)
23, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; 27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100; DB 1
Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB_1; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
       and for commercial
                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOTB_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                        Science 281:375-388(1998).
-!- FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR.
BE A LINKER THAT FASTENS THE TORQUE-GENERATING MACHINERY TO
                                                                                                                      Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T. McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOTB_TREPA
007887;
                                                                              "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
                                                                                                                 Venter J.C.;
                                                                                                                                                                                                                          MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      Limberger R.J., Slivienski L.L., El-Afandi M.C.T., Dantuono L.A., "Organization, transcription, and expression of the 5' region of fla operon of Treponema phagedenis and Treponema pallidum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
LIPID
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96345631; PubMed=8755894;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOTE OR TP0724
                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chemotaxis motB protein (Motility protein B).
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001145; Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S07952; S07952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EcoGene; EG11152; yfiB
                                                                                                                                                                                                                                                                                      a operon of Treponema phagedenis and Treponema pallidum. Bacteriol. 178:4628-4634(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
      CELL WALL (BY SIMILARITY).
SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 IPRSNLTTQGLGKKYPIASNKTAQGRAENRR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 INQASVEIISFGEERPIAFGTNEEAWSQNRR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X01818; CAA25961.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KLLPESQQQIQTMAAKLASTGLTHARMDGHTDNYGEDSYNEGLSLKRANVVADAWAMGGQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D90888; BAA16490.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 EIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRN-YLLGKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 APTGYTGVIYTG-----VAPLVDNDETVKALAS-----KLPSLVYFDFDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE000346; AAC75654.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 APLVFTSLILTGCQSPQGKFTP-----EQVAAMQSYGFTESAGDWSLGLSDAILFAKNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein; Signal; Complete proteome 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 AA; 17244 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%; Score 98.5; 23.8%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-ACYL DIGLYCERIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUTATIVE LIPOPROTEIN YFIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33FE5FBB174B7889 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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RESULT 36
MOTB_HELPY
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밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000930; Bac_OmpA; 1.
Chemotaxis; Flagella; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U28219; AAB61254.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                              STRAIN=2695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Mobi J.-F., White O., Kerlavga A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., Loftus B., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Lotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTB_HELPY STANDARD; PRT; 257 AA
P56427;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flagellar rotation; Complete proteome.

DOMAIN 1 14 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                             MOTB OR HP0816.
                                                                                                                                                                                                                                                                                                                                                                                                                         Chemotaxis motB protein (Motility protein B).
                                                  Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Helicobacter
                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori (Campylobacter pylori).
                                                                                                "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE MOTB FAMILY.
                                BE A LINKER THAT FASTENS THE TORQUE-GENERATING
 SUBCELLULAR
                                                FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 NRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TP0724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE001244; AAC65689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 VDNDETVKALASKLPSLVYFDFDSDEIK-PQAAAILDEQAQFLTTNQTA--RVLVAGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRRVDI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVEVPEDGSTD-NWELSTRRAVRVLHYLTDFGAQENRFSLAGYADTRAKFSNESPEGRAY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTSDE--RGLVISLTSDSFFYPGSSDLNVEESREALLRVAQFLSDHALAGRRFRIEGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQ 164
                 WALL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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5
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26050 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%; 29.4%;
Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95.5; DH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                       MACHINERY
     Inner membrane
                                                     MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         E:,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
 Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flagellar rotation; Complete proteome.

1 16 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pfam; PF00691; OmpA; 1.
proDom; PD000930; Bac_OmpA; 1.
Chemotaxis; Flagella; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; HP0816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - ! - SIMILARITY: BELONGS TO THE MOTB FAMILY.
                                                                                                                                        "Identification of genes involved in utilization of acetoin in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                  BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001145;
                                                                                                                                                                                                                                                                                                              01-FEB-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                       P39064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                          01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                   YTXE_BACSU
SEQUENCE FROM N.A
                                      Lapidus A., Galleron N., Sorokin A., I "Sequencing and functional annotation in the 200 kb rrnB-dnaB region.";
                                                                                            STRAIN=168;
                                                                                                                                    Mol. Microbiol. 10:259-271(1993).
                                                                                                                                                                                       MEDLINE=95020526; PubMed=7934817;
                        Microbiology 143:3431-3441(1997).
                                                                               MEDLINE=98048467; PubMed=9387221;
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      207
                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-TTNQTARVLVAGHTDE-----RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLVDNDETVKALAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGSTNPIAPNDSLENRMKNNRVEIFF 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQKLPKRVHINVRGFTDDTPLVKTRFKSHY--ELAANRAYRVMKVLIQYGVNPNQLSFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PASQNTETKATIARKGEGSVLEQIDQGSILKLPSNLLFENATSDAINQDMMLYIERIAKI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALFIALYAISAVNKSKVEALKTEFIKIFNYAPKPEAMQPVVVIPPDSGKEEEQMASESSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGEERPIAFGTNEEAWSONRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 AA;
                                                                                                                                                                                                                                                                                                               (Rel. 31,
(Rel. 31,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
                                                                                                                                                                                                                                                                                                  protein ytxE.
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
28849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bac_OmpA.
                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                             Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58C1774B0547C032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                               Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inner membrane;
                                                       Ehrlich S.D.;
n of the Bacillus subtilis genes
                                                                                                                                                                                                                                                                                                                                                                       242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KLPS-LVYFDFDSDEIKPQAAAILDEQAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 257;
                                                                                                                                                                                                                                                               Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                   acetate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Borvillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kunta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kunta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kunta K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Sekiguchi J., Sekowska A., Serco S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi A., Tanakoshi A., Tanaka T., Terpstra P., Togonoi A.,
RA Viaria A., Wedler E., Medler H., Weitzenegger T.,
RA Winters P., Willy A., Yamane K., Vasumoto K., Yata K.,
RA Winters P., Willy A., Yamane K., Vasumoto K., Yata K.,
RA Vasumoto K., Yata M., Yanane K., Osokikawa H., Danchin A.,
RA Vasumoto K., Y
                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subtilist; BG1036; ytxE.
Subtilist; BG1036; ytxE.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
ProDom; PD00930; Bac_OmpA; 1.
Hypothetical protein; Transport; Transmembrane; Complete proteome.
Hypothetical protein; Transport; Option Proteome.
1.
23
COMMAIN
1.
2.
COMMAIN
2.
COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997).

-I- FUNCTION: MAY BE INCLYED IN SOME TRANSPORT FUNCTION.
-I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-I- SIMILARITY: BELONGS TO THE MOTB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z99119; CAB14950.1; PIR; S39642; S39642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L17309; AAA68283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch).
183 AARASGVIQYFTSKEKLPSKRFIAVGYADTKPVKDNKTNEHMKENRRVEI
                                                                                                                                                         124
                                                                     122 ERRAVAVRNYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF008220; AAC00301:1; -.
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                          LQEAVLFDTGEAKVLKNAETLLHQIAVLLQTIPN-DIQVEGHTDSRNISTYRYPSNWELS
                                                                                                                                                                                                                   LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY----NMSLG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                               45
242 AA;
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               242
27595 MW;
                                                                                                                                                                                                                                                                                                                                   10.0%;
                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                   Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
; 8BA7DDC103C1DFF5 CRC64;
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                       0.94;
                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 242;
                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                            6,
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                              182
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RESULT 38

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MOTB_HELPJ
ID MOTB_H
AC Q9ZL29
DT 16-OCT
                                                                                                                                                                                                                                                                                                                                                         RESULT 39
                                                                                                                                                                 ОĀ
                                                                                                                                                                                                            Дb
                                                                                                                                                                                                                                           QΥ
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                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                   Query Match
Best Local
Q9ZL29;
16-OCT-2001 (Rel. 40, Created)
                                        MOTB_HELPJ
                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Cronin A., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucose-6-phosphate isomerase 2 (EC 5.3.1.9) (GPI 2) (Phosphoglucose isomerase 2) (PGI 2) (Phosphohexose isomerase 2) (PHI 2).
PGI2 OR SC01942 OR SCC54.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL035591; CAB38132.1; -.
HSSP; Q9N1E2; 1HOX.
InterPro; IPR001672; G6P_Isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00662; G6PISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: Involved in glycolysis and in gluconeogenesis -i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -i- SIMILARITY: BELONGS TO THE GPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z523;
                                                                                                                                                                                                                                                                                                                                                     Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
ACT_SITE 390 390 BY SIMILARITY.
ACT_SITE 514 SY SIMILARITY.
SEQUENCE 551 AA; 60569 MW; 631BD4A76EB34643 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00342; PGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G6P2_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphate.
                                                                                                                                                                   90 QAQFLTTNQTARVLVAGHTDERGSREYNMSLG 121
                                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.A.;
                                                                                                                                 MAGFADRVRTGE--WTGHTGRRIRNVVNIGIG 158
                                                                                                                                                                                                                                             QVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDE
                                                                                                                                                                                                        QELAAATGVSGLRDAMFRGERINITEDRAVLHTALRAPRDAVIEVDGENVVPQVHAVLDK
                                                                                                                                                                                                                                                                                 Conservative
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                               9.6%;
25.0%;
                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                 Score 83; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                               Mismatches
                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551
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                                                                                                                                                                                                                                                                                                 DB 1; Length 551 4.7;
                                        AA
                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                 COOS_RHORU
                                                                                                                                                                                            RESULT 40
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FRUM IN.A.

MEDLINE-99120557; PubMed-9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., I

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.

Smith D.R., Caruso A., Uria-Nickelsen M., Mills D.M., Iv

Tummino P.J., Caruso A. Mills S.D., Jiang Q., Taylor D.E.,
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Carbon monoxide dehydrogenase (EC 1.2.99.2) (
                                                                                                             P31896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plagellar rotation; Complete proteome. Plagellar rotation; Complete proteome. Plagellar 16 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                        COOS_RHORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000930; Bac_OmpA; 1.
Chemotaxis; Flagella; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastric pathogen Helicob
Nature 397:176-180(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemotaxis motB protein MOTB OR JHP0752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001506; AAD06331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic sequence comparison of two unrelated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane SIMILARITY: BELONGS TO THE MOTE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE A LINKER THAT FASTENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR.
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42; Conserv
                                                                                                                                                                                                                                                                           YGSTNPIAPNDSLENRMKNNRVEIFF 232
                                                                                                                                                                                                                                                                                                                          FGEERPIAFGTNEEAWSQNRRAELSY 172
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257 ₽
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                                                                                                                                     STANDARD;
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28838 MW;
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a; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Motility protein
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
PERIPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                     A
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        (CODH)
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, Ives C.
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                        Pfam; PF03063; Prismane; 1.
Oxidoreductase; Nickel; Iron; Zinc; Iron-sulfur.
METAL 50 50 IRON-SULFUR (BY SIM
METAL 53 53 IRON-SULFUR (BY SIM
METAL 72 72 IRON-SULFUR (BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. - i - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Rhodospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhodospirillum rubrum and the gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fox J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and physiological characterization rubrum carbon monoxide dehydrogenase system.
J. Bacteriol. 174:5284-5294(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92355502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodospirillum rubrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- INDUCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96198151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=URI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roberts G.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kerby R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POX J.D., Kerby R.L., Roberts G.P., Ludden P.W.; ^{\circ}CO-tolerant hydrogenase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDUCTION: By carbon monoxide; under anaerobic conditions. MISCELLANEOUS: METHYL VIOLOGEN CAN ACT AS ACCEPTOR. SIMILARITY: STRONG, TO C. HERMILACETICUM CARBON MONOXIDE DEHYDROGENASE BETA SUBUNIT AND SOME, TO M.SOEHNGENII CARBON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MONOXIDE DEHYDROGENASE ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                   ; U65510; AAC45123.1; C42957; C42957.
                            132
                                                                                                                       522
                                                                                                                                                     52
                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                  YVDLAKSLAKRNYLVLATGCAAGAFAKAGLMTSEATTQYAGEGLKGVLSAIGTAAGLGGP
RAGLGL 639
                            LLGKGI 137
                                                                                                                     LPLYMHMGSCVDNSRAV-ALATALANKLGVDLSDLPLVASAPECMSEKALAIGSWAVTIG
                                                                                                                                                                                                                HIQIAAAAALSVLTFMTGCANKSTSQV-MVAPNAPTGYTGVIYTGV---
                                                          LPTHVGSVPPVIGSQIVTKLVTETAKDLVGGYFIVDTDPK-----SAGDKLYAAIQER
                                                                                                                                                                                                                                                                                                                                                                                                   IPR004137; Prismane.
                                                                                                                                                                                                                                                                                                           639
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                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CODH MAY OXYDATE CARBON MONOXIDE COUPLED, VIA COOF, TO OF HYDROGEN CATION BY AN HYDROGENASE (POSSIBLY COOH).

ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
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                                                                                                                                                                                                                                                                                                          AA;
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                                                                                                                                                     -VDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQA-
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                                                                                                                                                                                                                                                                                                           66854 MW;
                                                                                                                                                                                                                                                           9.4%;
                                                                                         -QFLT--TNQTARVLVAGH----TDERGSREYNMSLGERRAVAVRNY 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                             Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                        IRON-SULFUR (BY SIMILARITY).
IRON-SULFUR (BY SIMILARITY).
IRON-SULFUR (BY SIMILARITY).
; DCADD7C13D8D85B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision; Rhodospirillaceae;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coppoc
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8.6;
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                                                                                                                                                                                                                                                                           Length 639
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Search completed: July 6, 2003, 14:05:18 Job time : 39 secs

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Listing first 100 summaries
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                            289
287.5
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269.5
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2: sp_barcteria
3: sp_fungi:*
4: sp_human:*
5: sp_nammal:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_blant:
11: sp_rodent
12: sp_virus:
13: sp_verteb
14: sp_unclas:
15: sp_varche:
17: sp_arche:
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sp_unclassified:*
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                                             09i4zi pseudomonas
09xfhf salmonella
093495 erwinia chr
08ylf4 ralstonia s
09a3h5 caulobacter
08zgz0 yersinia pe
098f85 rhizobium l
09pc85 xylella fas
0926c3 rhizobium m
08u915 agrobacteri
09kr12 vibrio chol
09zch2 rickettsia
               Q9zch2 rickettsia
Q44662 brucella ab
Q44157 actinobacil
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Q8RML9
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Q9X4R6
Q9XCZ4
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Q9SSJ9
Q9SSJ9
Q9SOKG
65 Q9CMNI
086254
Q9X4R9
Q51778
Q52465
Q9X4S0
Q9PMI4
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6 Q8HSYB
6 Q8USS
6 Q8YHI1
7 Q9X4R
7 Q9X4R
7 Q9X4R
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09XCZ3
09XCZ3
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Q8VR19
Q46099
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6 Q9Z7C5
Q9ZST9
           Q9K538 rhodospiril
Q9X476 pseudomonas
Q9xcz4 pseudomonas
Q8rmm2 haemophilus
Q8rmm0 haemophilus
Q8rmm0 haemophilus
Q8rm19 haemophilus
Q8rm19 haemophilus
Q8rm19 haemophilus
Q8rm10 haemophilus
Q8rm10 haemophilus
Q8rm10 haemophilus
Q8rm10 haemophilus
Q8rm10 haemophilus
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Q9abm6 caulobacter
Q9s6b8 pseudomonas
Q8reh8 fusobacteri
Q9a2r2 caulobacteri
Q9a2r2 caulobacteri
Q9a4r3 pseudomonas
Q9s5j9 actinobacil
Q9x463 pseudomonas
Q9x66 shewanella
Q9xm1 pasteurella
Q9xm1 pseudomonas
Q9x4r9 pseudomonas
Q9x4r9 pseudomonas
Q9x480 pseudomonas
Q9x480 pseudomonas
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Q52465 pseudomonas
Q52465 pseudomonas
Q9x4s0 pseudomonas
Q9pm14 campylobact
Q9k558 rhodospiril
Q9x4r6 pseudomonas
Q9xcz4 pseudomonas
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O8rgn8 fusobacteri
O31154 vibrio chol
O51777 pseudomonas
O48265 haemophilus
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O9x4s1 pseudomonas
O9x4s1 pseudomonas
O9i5a7 pseudomonas
O9i5a7 pseudomonas
O9i5a7 pseudomonas
O9x691 helicobacte
O51780 pseudomonas
O51721 pseudomonas
O9x695 pseudomonas
O51721 pseudomonas
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Q9x4r7 pseudomonas
Q9wwi5 pseudomonas
Q8r6jl fusobacteri
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Q92705 chlamydia p
Q92st9 rhizobium m
Q98na9 rhizobium n
Q8vr19 myxococcus
Q46099 campylobact
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Q8ubx6 agrobacteri
Q8xrs0 ralstonia s
Q8yhl1 brucella me
Q8re60 fusobacteri
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Q9hzu7 pseudomonas
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Q92gc3 rickettsia
Q45017 bartonella
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Q8xwu0 ralstonia s
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Q9pje0 chlamydia m
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025750 helicobacte
Q9zk87 helicobacte
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RESULT 1

Q51489
ID Q5149
ID Q514
DT Q1-J
DT Q
RESULT 2
Q914Z4
ID Q914
AC Q914
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Q11489;
Q1-10V-1996 (TrEMBLrel. 01,
Q1-JAN-1998 (TrEMBLrel. 05,
Q1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer-membrane peptidoglycan associated lipoprotein (PAL) of pseudomonas aeruginosa."; Microbiology 143:1709-1716(1997).
EMBL; Z50191; CAA90573.1; -.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97312009; PubMed=9168620;
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                                                                   01-MAR-2001 (TIEMBLIEL. 16, Created)
01-MAR-2001 (TIEMBLIEL. 16, Last seg
01-MAR-2002 (TIEMBLIEL. 20, Last ann
                       Outer membrane protein OprL OPRL OR PA0973.
                                                                                                                   Q9I4Z4;
01-MAR-2001
                                                                                                                                                           Q914Z4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 35.7%; Score 307; Local Similarity 40.9%; Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158.5
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                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                     120 LGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                  62 RAITT----FYFEYDSSDLKPEAMRALDVHAKDL-KGSGQRVVLEGHTDERGTREYNMA 115
                                                                                                                                                                                                                                                                                                                                                                                                           60 KALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 QIAAAAAALSVLTFMTGCANK-----STSQVMVAPNAPTGYTGVIYTGVAPLVDNDETV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFAALALAMAV---AVGCSSKGGDASGEGANGGVDPNA--GY-GANSGAVDGSLSDEAAL 61
                                                                                                                                                                                                                                                                                 LGERRAKAVQRYLVLQGVSPATLELVSYGKERPVATGHDEQSWAQNRRVEL 166
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                                                                                                                                                                PRELIMINARY;
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Q9KLT2
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006895
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P96774
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Q52584
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Q9X4L6
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                                                                          Last sequence update)
Last annotation update)
                                                    precursor.
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006895 campylobact
Q9x4s2 pseudomonas
Q9x416 pseudomonas
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Q8rjd0 haemophilus
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Q52584 pseudomonas
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RESULT 3
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Best Local S
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Nature 406:959-964(2000).

EMBL; AE004530: AAGNA767
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STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
STOVET C.K., Pham X.-Q.T., Erwin A
STOVET C.K., Pham X.-Q.T., Erwin A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000930; Bac_OmpA; 1. PROSITE; PS01068; OMPA; 1.
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Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9XFH6;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tol protein required for outer membrane integrity, uptake
Tolicins, and translocation of phage DNA to cytoplasm
(Peptidoglycan-associated lipoprotein).
PAL OR STM0749 OR STY0795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                               McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                          SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium, and Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8XFH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
   SPECIES-S.typhi; STRAIN-CT18;
                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602, 601;
                                                                                            Nature 413:852-856(2001).
                                                                                                                                                    Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 LGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RAITT-----FYFEYDSSDLKPEAMRALDVHAKDL-KGSGQRVVLEGHTDERGTREYNMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 KALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 QIAAAAAALSVLTFMTGCANK-----STSQVMVAPNAPTGYTGVIYTGVAPLVDNDETV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 306; DB 16; Length 168; Pred. No. 9.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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O934G5
AC OSS
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Best Local :
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Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; 1.
Lipoprotein; Complete proteome.
                                                                                                                                                                                                                                                                                     Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.; "Characterization of the Erwinia chrysanthemi tol-pal gesubmitted (CCT-2000) to the EMBL/GenBank/DDBJ databases EMBL; AJ297885; CAC82710.1;
                                                                              SEQUENCE
                                                                                                                                                                             ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; UNKNOWN_1.
                                                                                                                                                                                                                                         InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                       Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pectobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptidoglycan-associated lipoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q934G5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE008730; AAL119693.1; -. EMBL; AL627268; CAD05211.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitehead
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 33.6%;
Local Similarity 36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 RGTPEYNISLGERRANAVKMYLQGKGVSADQISIVSYGKEKPAVLGHDEAAYAKNRRAVL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 VY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 SY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 MSSEEQARLQMQQLQQNNIYYFDLDKYDIRSDFAAMLDAHANFLRSNPSYKVTVEGHADE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MQLNKVLKGLMIALPVMAIAACSSNKNASN------DGSEGGMLNGAGTGMDANGNGN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MMLHIQIAAAAAALSVLTFWTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NDETVKALASKLP--SLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                        168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 AA; 18865 MW; A515624F96EBB5A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.6%; Score 289; DB 16; Length 174; ilarity 36.8%; Pred. No. 3.7e-19; Conservative 33; Mismatches 64; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                 21
                                                                     18433 MW;
   33.4%; Score 287.5;
                                                                                  PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN
                                                                                                                        POTENTIAL.
                                                               1E315BCF52852DD5 CRC64;
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   DB 2;
                                                                                                                                                                                                                                                                                                                                                        tol-pal genes.";
Length 168
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AC ID
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Q9A3H5;
               Q9A3H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisane N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 172 AA; 18656 MW;
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01068; OMPA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
EMBL; AL646060; CAD14266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=GMI1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable peptidoglycan-associated lipoprotein precursor. PAL OR RSC0736 OR RS05117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000104; Antifreeze_1.
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8Y1F4;
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                                                                                                                                                                                                                                                                                                                   Local
                                                                                                123
                                                                                                                   123 RRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSONRRAELSY 172
                                                                                                                                                               63
                                                                                                                                                                                   63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 SIGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                   5 IQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTG-YTGVIYTGVAPL-VDNDETVKAL 62
                                                                                                                                                                                                                    8 IKLAAIAALLALGACSSGVKLDDTSK-----NATGGAAAGADTRNVTPVDVSRDELTDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 LOMOELORNNIVYFDLDKYDIRPDFAQMLDAHAAFLRSNPSYKVTVEGHADERGTPEYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ALASKLP--SLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LMLALPVLAVAACSS------NKHANNDQSSLNGGAGMEN-----GGNMSSAEQAR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
                                                                                      KRAEAVRRALSSLGVPDSQMESVSLGKEKPQASGHDEESWAQNRRSDIVY 172
                                                                                                                                                     SPLAKRSVYFDFDSYTVKPEYQGLLTQHARYLQSHNQRKVLIQGNTDERGTSEYNLALGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALGERRANAVQMYLQGKGVSADQISVVSYGKEKPAVLGHDEAAWSKNRRAVLVY 168
            PRELIMINARY;
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                        33.3%; Score 286.5;
38.2%; Pred. No. 6.3e
tive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.9e-19;
            PRT;
                                                                                                                                                                                                                                                                                                                                                        5CFF28E6AE7702D9 CRC64;
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          188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 AA.
                                                                                                                                                                                                                                                                                                      6.3e-19;
                                                                                                                                                                                                                                                                                                                      DB 16; Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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       RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-ATCC 19089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=155892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE005987; AAK25191.1; -.
MEDIJUNE 21/70/413; PubMed=11586360;
MEDIJUNE 21/70/413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague."
                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Peptidoglycan-associated lipoprotein Pal.
                                                                                                                                                                                                                                                                                                                                                                              Q8ZGZ0;
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                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                             PAL OR YPO1125
                                                                                                                                                                                                                                                                                                                                                                                                     Q8ZGZ0
                                                                                                                                                                 STRAIN=CO-92 / BIOVAR ORIENTALIS;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=632;
                                                                                                                                                                                                                                       Yersinia
                                                                                                                                                                                                                                                                          Yersinia pestis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSVQDFVVNIGDRVYFDTDEYVIRADAQPVLAGQAQWLNRYSSVRIRIEGNADERGTREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLALGARRANAVRDFLIAQGVSSARIETISFGKERPIDPGSSEEAWAKNR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGLAAASLA----ACASRPKPQPVTPPPAQPQPTQPTPYTPPAPPPVTSGILP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%; Score 286.5; 38.2%; Pred. No. 7.1
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                                                                                                                                                                                                                                                         gamma
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                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                           subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                      168
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                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 188;
       agent of plague.";
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RESULT 8
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Best Local :
                                                                                                                                                    Matches
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Lipoprotein; Complete proteome.
SEQUENCE 168 AA; 18084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:523-527(2001).
EMBL; AJ414146; CAC89968.1; -
InterPro; IPR001145; Bac_OmpA.
pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa; 1.
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01-OCT-2001 (TrEMBLrel. 18, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein ml13887.
                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa
Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q98F85
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q98F85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                               proDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 168 AA; 17765 MW; 03E260D3BA1ECBB3 CRC64;
                                                                                                                                                                                                                                                                          Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                    DNA Res.
                                                                                                                                                                                                                                                                                                                                  Mesorhizobium loti.
                                                                                                                                                                                                                                                                                                                                                 "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                 Takeuchi C., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                             Mochizuki Y.,
                                                                                                                                                                                                                                                            PRINTS; PR01021; OMPADOMAIN
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130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                       es. 7:331-338(2000).
AP003003; BAB50682.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MQLNKVLKGLMLALPVLAVAACSSNKSANNDQSGMGAGTG-----TENGSNLSSEEQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                           61 IFFDTDSSSIRADAQTTLARQAQWLNQYKQYAIVVEGHADERGTREYNLALGARRAAAAR 120
                                                       70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                       15 ALVAMLAIAGCASKKT-----PNNAADLGLNG---AGAATPGSAQDFTV-----NIGDR 60
                                                                                                                    13 ALSVLTFMTGCANKSTSQVMVAPN--APTGYTGVIYTGVA-PLVDNDETVKALASKLPSL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQMQELQKNNIVYFGFDKYDIGSDFAQMLDAHAAFLRSNPSDKVVVEGHADERGTPEYNI
                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                    Nakayama S., Nakazaki N., Shimpo S., Yamada M., Tabata S.;
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                                                                                                                                                                    31.3%;
40.3%;
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                                                                                                                                                       25;
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                                                                                                                                                                    Score 269.5; DB 1
Pred. No. 2.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3AAA851E765F1994 CRC64;
                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 283; LL
NO. 1.3e-18;
68
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                                                                                                                                                                                       DB 16;
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                                                                                                                                                         53; Indels
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                                                                                                                                                                                      Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Kimura T.,
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.R.P., Camargo A.A., Canargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.
RA Coutlinb L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Fracincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Pranco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Lalgret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira M.M.F., Matsukuma A.Y.,
RA Macnado M.A., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manna A. Jr., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA de Silva A.C.R., da Silva A.M., Varjovski-Almeida S., Vettore A.L.,
"The qenome sequence of the blant bathoden X.Jella fastidica ".
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Best Local
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Pfam; PF00691; Ompa; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_Ompa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AB004009; AAF84702.1; -.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20365717; PubMed=10910347;
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                 137
                                                           126 VAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
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                                                                                                                                                                                                                                                            26 LVACSKKVKEQPHVPVKTMAPTVSTPAPTTTAPTDSSG-LYT--AADLDTDACLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                      LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                           MTGCANKSTSQVMV------AP--NAPTGYTGVIYTGVAPLVDNDETVKALASK 65
NSVLYSLQANGASSGQLNVVSYGEERPVCTESTESCWSRNRRVEIVY 183
                                                                                                                              -QRVVYFDFDKDDVKKEFQTVLGCHAKYLRNRPSAHITLQGNTDERGSREYNIALGERRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20431 MW; C8DD2F6233DB0C92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     30.8%; Score 265.5; 35.9%; Pred. No. 6.3
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                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogen Xylella fastidiosa."
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RESULT 10
Q926C3
ID Q926C
AC Q926C
DT Q1-DE
DT Q1-DE
DT Q1-DE
DT Q1-DE
DT Q1-DE
CO PAL Q
OS Rhizo
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RP SEQUE
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RA Capel
RA Godri
RA Godri
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Best Local :
SEQUENCE FROM N.A.

MEDLINE-21608550; PubMed=11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.

Chen Y., Enou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry
                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Botstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizoblum meliloti strain 1021.", Sinorhizoblum meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Rhiz
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALA OR ATU3713 OR AGR_L_2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omp16 protein
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00691; OmpA; 1.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable peptidoglycan-associated lipoprotein precursor. PAL OR R02738 OR SMC02942.
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01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 VSRGVPGNRMRTISYGKEKPVAVCDDISCWSQNRRA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 LGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 DTDSTSIRADAQATLDRQAQWLAKYPNYGITIEGHADERGTREYNLALGARRAAATRDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 ALVMTLALAGCASKKN-----LPNDAAG-LGLGAGAATPGSQQDFTV-----NVGDRIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 DFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 ALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18735 MW; A6F162CB35042268 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%;
         Biddle P., Jung M., Krespan W., Perry M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 262.5; DB 1
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bothe G., Ampe F., Batut J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 176;
                                                                                                                                                                                                                                                                                                                                                                            33970).
Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                               Jr., Woo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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Mon

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RESULT 12

Q9KR12

ID Q9KR1

AC Q9KR1

DT 01-OC

DT 01-OC

DT 01-DC

CT 01-DC

GN Vibr

GN Vibr

RN [1]

RN [1]

RN [1]

RN ETI

RA Hei

RA Hei

RA Gil

RA Gil

RA Gil

RA ETI

RA FT

DR TT

DR T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;

"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefactens C58.";

Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chumley F., Tingey
Nester E.W.;
"The genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-EL TOR N1691 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers I

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., White O.,

McDonald L., Utterback T., Fleischman R.D., Nierman W.C., White O.,

McDonald L., Utterback T., Fleischman R.D., Nierman W.C., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TremBLrel.
01-OCT-2000 (TremBLrel.
01-DEC-2001 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21608551; PubMed=11743194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2317-2323(2001).
                                                                                                                                                                                             Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptidoglycan-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9KR12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9KR12
                                                          InterPro; IPR001145;
Pfam; PF00691; OmpA;
                                                                                                                                                           cholerae
                                          PRINTS; PR01021; OMPADOMAIN.
                                                                                                                                        Nature 406:477-483(2000).
                                                                                                                                                                             "DNA sequence of both chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE009302; AAL44523.1; -. AE008312; AAK89692.1; -.
                                                                                                  VC1835;
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                                                                                                                    AE004259; AAF94983.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                      PD000930;
      PD000930; Bac_OmpA; 1. PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIFFDTDSTSIRADAQQTLQRQAQWLSRYPNYAITVEGHADERGTREYNLALGARRAAAT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVIAMTLALAGCANKKN-----MPNS-AGELGLGGAGSATPGSQQDFTV----NVGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDFLASQGVPASRMKTISYGKEKPVAVCDDISCWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18839 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.4%; Score 262; DB 16; 38.1%; Pred. No. 1.3e-16;
                                                                            Bac_OmpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15, Created)15, Last sequence update)19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A3AB53402ECB1ADD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                               of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                         Sellers P.,
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RESULT 13
Q9L3Q8
                                                                                                                             RESULT 14
Q9ZCH2
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Best Local
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein; Complete proteome. SEQUENCE 172 AA; 18491 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goswami P.P., Chaudhuri P., Grish K.S.; "cloning and sequencing of the gene encoding a 16 kDa outermembrane protein of Pasteruella maltocida p52."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ271673; CAB75338 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                      Q9ZCH2;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 1)
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001145; Bac_OmpA. pfam; pF00691; OmpA; 1. PR10175; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9L3Q8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMP 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9L3Q8
                                                                                                                  Q9ZCH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-P52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
               Rickettsia prowazekii.
                                          Peptidoglycan-associated lipoprotein precursor (PAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                    130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                       88 HYLSAKGVQAGQVSTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 130
                                                                                                                                                                                                                                                 28
                                                                                                                                                                                                                                                                          70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MQLNKVLKSLLIALPVLA-VTACSSSDDAANSGSQTNQSAVSTVDSNGLNAQGQL----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MMLHIQIAAAAAALSVLTFMTGC----ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNIALGERRAQAVAKYLEALGVQAGQLSIVSYGEEKPLVLGQSEEAYAKNRRAVLVY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQELKEQALRENQTIYFAFDNATIASDYEAMLAAHAAYLVKNPSLRVTIEGHADERGTPE
                                                                                                                                                                                                                  NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                               VYFGFDKYNIEGEYVQILDAHAAFLNATPATKVVVEGNTDERGTPEYNIALGQRRADAVK
                                                                                                                                                                                                                                                                                                                                                              130 AA;
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                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                              14216 MW;
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                                                                                                                                                                                                                                                                                                                      30.0%;
48.5%;
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                                                                                                                                                                                                                                                                                                          19;
                                                          Last sequence update)
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Pred. No. 2.3e-16;
                                                                                        Created)
                                                                                                                                                                                                                                                                                                                      Score 258; DB 2;
Pred. No. 1.9e-16;
                                                                                                                                                                                                                                                                                                                                                                 91E7D2C2A9A87F44 CRC64;
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                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision;
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ACCOMPANDATION OF THE PROPERTY OF THE PROPERTY
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Q44662
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Best Local Similarity
SPECIES=B.melitensis; STRAIN=16M / ATCC 23456 / BIOTYPE MEDLINE=20020109; PubMed=11756688;
                                                                                                                                                             Tibor A., Aidant N., Letesson J.;
"The tol-pal region in Brucella e
of E. coli.";
                                                                                                                                                                                                                                                                                                                                       Tibor A., Weynants V., Denoel P., Lichtfouse B., De Bolle X., Saman E., Limet J.N., Letesson J.J.;
"Molecular cloning, nucleotide sequence, and occurrence of a 16.5-kilodalton outer membrane protein of Brucella abortus with similarity to pal lipoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                             SPECIES=B.melitensis; STRAIN=16M / ATCC 23456 / BIOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=B.abortus 1, and B.melitensis; STRAIN=544, AND 16M; MEDLINE=94341863; PubMed=8063379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMP16 precursor (PAL protein) (Peptidoglycan-associated
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brucella melitensis.
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    Infect. Immun. 62:3633-3639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=35802,
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EMBL; AJ235273; CAA15198.1; -.
InterPro; IPR001145; Bac_OmpA.
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PRINTS; PR01021; OMPADOMAIN.
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Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
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"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-MADRID E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 LANKGIAHNRLNTISYGKDKPAMIGNTEEAFSYNRRA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 LIGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 FAFDSSSLSPKAKEELERQACWLSKHPEVKVTVEGHCDERGTREYNLALGERRAAAAKQF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 FDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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                                                                                                             (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                region in Brucella encodes homologs of the Tol-Pal system
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                                                                                                                                         ProDom; PD000930; Bac_OmpA; 1.

PALA OUTER MEMBRANE PROTEIN.
                                                                                                                                                                                                             outer membrane protein belonging to the family of PAL Res. Microbiol. 147:351-361(1996). EMBL; X89009; CAA61413.1; -. InterPro; IPR0011145; Bac_OmpA.
                                                                                                                                                                                                 Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-96298014; PubMed-8763621;

Frey J., Kuhnert P., Villiger L., Nicolet J.;

"Cloning and characterization of an Actinobac

"Cloning and characterization of the famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                       Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
                                                                                                                                                                                                                                                                                                                                                                                                                                              PALA outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=715;
                                                                                                                                                                                                                                                                                                                                                                                    Actinobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
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                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 MSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 LALGORRAAATRDELASRGVPTNRMRTISYGNERPVAVCDADTCWSQNRRA 159
8 LMIAAPA-----FVLAACSSSSDNANANANAGQFGGM-----TAEDLQT 48
                              5 IQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 TV-----NVGDRIFFDLDSSLIRADAQQTLSKQAQWLQRYPQYSITIEGHADERGTREYN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF358662; AAK48919.1; -. AE009476; AAL51521.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L27996; AAA59360.1;
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                                                                                       Similarity
                                                                                                                                                                                  PR01021; OMPADOMAIN.
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                                                                                                                                     152 AA;
                                                                        Conservative
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                                                                                                                                    16235 MW;
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36.3%;
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                                                                      27;
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Pred. No. 6.5e-16;
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                                                                                                                                  892C1E23E80406A7 CRC64;
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                                                                                                 DB 2;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=85-02323;
MEDLINE=96239002; PubMed=8675292;
Spinola S.M., Hiltke T.J., Fortney K., Shanks K.;

*The conserved 18,000 molecular weight outer membrane protein
Haemophilus ducreyi has homology to PAL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus ducreyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q47958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1. SEQUENCE 157 AA; 17051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 64:1950-1955(1996).
EMBL; U42466; AAC44382.1; -.
                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q92GC3
Samson
Raoult
                      Ogata H., Audic S., Renesto-Audiffren P., Samson D., Roux V., Cossart P., Weissenba
                                                                                                     SEQUENCE FROM N.A. STRAIN-MALISH 7;
                                                                                                                                                                                                                                                                                           Peptidoglycan-associated lipoprotein PAL OR RC1200.
                                                                                                                                                                                                                                                                                                                                                                                                                               Q92GC3;
                                                                                                                                                                                NCBI_TaxID=781;
                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                  Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                              MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                               Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kDa outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE
0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADAVKNYLATKGANQVST--VSYGEEKPAVLGHTEADYAKNRRAVLEY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RY-NTVYFGFDSYAVEGEYQQLLDAHAAYL-TSANGKVTVAGHADERGTPEYNIALGQRR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTRY-NTVYFNFDSYAVEGEYRQLLDAHAAYLTSS-NSKVTVTGHADERGTPEYNIALGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMIAAPAFVLTACSSSSGKTDANANMNGDAMAVNQFGGM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQIAAAAAALSVLTFMTG--CANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRADAVKNYLATKGVSQVST--VSYGEEKPSVLGHTEADYAKNRRAVLEY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001145; Bac_OmpA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                     alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 246; UD ...
No. 3.3e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                              Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 AA
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                                 Fournier P.-E., Barbe
ch J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                 Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                             Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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DT DT DE

Peptidoglycan

associated lipoprotein precursor

(OMP18).

O25750 PRELIMINARY; PRT; 179 AA.
025750;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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RESULT 19
Q45017
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RESULT 20
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Best Local
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                                                                                                                                                                             Query Match
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ProDom; PD000930; Bac_ompA; 1.
Lipoprotein; Complete proteome.
SEQUENCE 155 AA; 17340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
EMBL; AE008667; AAL03738.1; ..
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, 10-DEC-2001)
                                                                                                                                                                                                       PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; UNKNOWN_1
SEQUENCE 171 AA; 19334 MW; 3A
                                                                                                                                                                                                                                                                                                                                                                                                                    Bartonella bacilliformis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q45017;
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                                                                                                                                                                                                                                                                EMBL; L47642; AAA78948.1; -.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                       Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                          Bartonellaceae; Bartonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                18.5 kDa protein
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Arevalo J.I., Williams M.L.,
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=774;
                                                                                                                                                                                                                                                                                                                                    "Anonymous DNA sequence with ORF from
                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 GLGERRAAAKKFLAHKGIDHNRLNTISYGKDRPAMMGNTEEAFAYNRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 SLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSONRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
                                                                    130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 VKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM
                                          93 DYLVSLGVSPQRMKTMSYGKERPVAVCDDISCWNQNRRVVIS
                                                                                                33
                                                                                                                        70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 KITLAFLALCVL---AGCNT-------TKRAPQFDGNMNQSEETSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVD-----NDET--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKDFEKHAGNAVWFAFDSSALSPKAKEELERQACWLSKHPEVKVTVEGHCDERGTKEYNL
                                                                 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                              VFFSLDSSVIEADAQRILVRQAEWLLLYPHHTIMIEGHADDRGTREYNLALGQRRAIAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.2%;
35.9%;
                                                                                                                                                                   27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                       alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 6.
                                                                                                                                                                    Score 235; DB 2; Pred. No. 3.9e-14;
                                                                                                                                                                                                                                                                                                                                                       Marks K.L., Ihler G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58E05C7E8F027A84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                              3A156E3F8FF24DBE CRC64;
                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
                                                                                                                                                                                                                                                                                                                                       Bartonella bacilliformis
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                                                                                                                                                                                   Length 171;
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                                              134
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Q9ZK87
AC Q9ZK87
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Best Local Similarity
                                                                                                                                                                                               MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C. Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
                                                         gastric pathogen Helicobacter pylori.", Nature 397:176-180(1999).
                                                                                                                                                               Trust T.J.;
                                                                                                                                                                            Gibson_R., Merberg D., Mills S.D., Jiang Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TIEMBLIEL. 10, Created)
01-MAY-1999 (TIEMBLIEL. 10, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation updat
                                   EMBL; AE001533; AAD06633.1; -.
                                                                                                                  "Genomic sequence comparison of two unrelated isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Lipoprotein;
SEQUENCE 179 AA; 19978 MW; 5B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Janes P.D., Smith H.O., Fraser C.M.,
            InterPro;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ZK87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q92K87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; HP1125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000619; AAD08169.1; -.
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MEDLINE=97394467; PubMed=9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 SVLTFM------TGCANKSTSQVMVAP-NAPTGYTGVIYT-------GVAPLVDND 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFSFLVAFLLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 215.5; DB 16; Length 179; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sin; Complete proteome.
5B5521E284E27B4C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                         Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
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                                                                                                                  of the human
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Q9ZAW7
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       Q8XWU0;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ZAW7;
Q9ZAW7;
01-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                    Q8XWU0
                                                                                                                                                                                                                                                                                                                                                                                                        Seo W.Y., Kim J.S., Jang J.H., Yu G.J., Yum J.; submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U75869; AADD9577.1; ... InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
SEQUENCE 179 AA; 20024 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=KCTC0217BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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                                                                                                                                                             122 ERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVQKTRECYRENRRVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                   62 LASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLG
                                                                                                                                                                                                                                             10 LVAFLFTAGCKHNMDKETVAGDVSAKAVQSAPVSTETAQEKQEPKQEPAPVVEEKPAVE- 68
                                                                                                                                                                                                                                                                          14 LSVLTFMTGCANKSTSQYMVAP-NAPTGYTGVIYTGV-----APLVDNDETVKA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 PAIE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
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                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                    VKRTLSVKNALVIKGVEKDMIKTISFGETKPKCTQKTRECYKENRRVDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                        -SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEYNQALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY
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) (TrEMBLrel. 10,
L (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA; 20030 MW; F62BB6191864588D CRC64;
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                            Conservative
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32.8%;
                                                                                                                                                                                                                                                                                                                      24.2%; Score 208.5; 30.8%; Pred. No. 1.2
                                                                                                                                                                                                                                                                                                            33;
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                       Last
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Last annotation update)
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                      sequence update)
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Probable

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Last annotation update)

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Query Match
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RMBL; AL646669; CAD16087.1; "Genome Sequence Of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSC2380 OR RS01165.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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Pfam; PF00691; OmpA; 1.
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                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=305;
                                                                                                                                                                                                                                                       Helicobacter pylori (Campylobacter pylori)
Bacteria; Proteobacteria; epsilon subdivis
                                                                                           "Identification of Helicobacter pylori Antigens.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF181881; AAF04276.1;
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                     Q9RNF4;
                                                                                                                                                                                                                                                                                                                                                                                    Q9RNF4
                                 PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
SEQUENCE 157 AA; 17536 MW;
                                                                                                                                                                            STRAIN-RU-1
                                                                                                                                                                                            SEQUENCE FROM N.A.
                               SEQUENCE
                                                                                                                                                             Kolesnikow T., Gekas S., Lee A.;
                                                                                                                                                                                                                         NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 RMSAEGRGQTQPVGDNATEAGRAQNRRVEI 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                PF00691; OmpA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 GGALGAAGGAAVGYNWNAIKSKLTGDTAGTGTQISEQPDGSLKLNIPSQVSFDTDSAVIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MLHIQIAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21174 MW;
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27.6%; Pred. No. 2.4
     23.9%;
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                                                                                                                                                                                                                                                          epsilon subdivision; Helicobacter group;
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Last annotation updat
   Score 205.5;
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                                    E7FB05D3C4E5641C CRC64;
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      Length 157;
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Best Local S
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PEPTIDOGLYCANE associated lipoprotein precursor (Peptidoglycan associated lipoprotein) (OMP18).
OMP18 OR PAL OR CJ0113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE-96121222; PubMed-8576327;
Burnens A., Stucki U., Nicolet J., Frey J.;
"Identification and characterization of an immunogenic outer membrane protein of Campylobacter jejuni.";
J. Clin. Microbiol. 33:2826-2832(1995).
                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q46123
                                                                                                                                                                                                                 PRINTS; PRO1021; OMPADOMAIN.

ProDom; PD000930; Bac_OmpA; 1.

Signal; Lipoprotein; Complete proteome.

SIGNAL 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                            reveals hypervariable sequences.";
Nature 403:665-668(2000).
EMBL; X83374; CAA58288.1; -.
EMBL; AL139074; CAB72597.1; -.
Interpro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q46123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=197;
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 V 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 L 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 APVVEEKPAVE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 APLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
35 NRGSGGSDGWDIDSKISQLNDTLNKVYFDFDKFNIRPDMQNVVSTNANIFNTEVSGVSIT
                                                            4 ILFTSIAALAVVIS-----GCSTKSTS---
                                                                                         2 MLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFGSSEYNQALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVD
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERGSREYNMSLGERRAVAVRNYLLGKGINQASVBIISFGEERPIAFGTNEEAWSQNRRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                       165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.0%;
                               --LASKLPSL------VYFDFDSDEIKPQAAAILDEQAQFLTTNQT-ARVL 103
                                                                                                                                                                                        17829 MW;
                                                                                                                                           23.8%; Score 204.5; DB 30.1%; Pred. No. 2.6e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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5; Mismatches
                                                                                                                                                                                                         PEPTIDOGLYCANE ASSOCIATED LIPOPROTEIN
                                                                                                                                                                                          24CA7928532C2B66 CRC64;
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                         DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                               58;
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                                                                                                                               Indels
                                                                                                                                                         Length 165;
                                                                    --- VSGDSSVDS
                                                                                                                               47;
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Q9Z7C5
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Best Local :
                                                                                                                                                                                                                                                                                                                                                  InterPro; 1: CompA; 1.
Pfam; Pf00691; OmpA; 1.
ProDom; PD000930; Bac_OmpA; 1.
Lipoprotein; Complete proteome.
192 AA; 21925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Linher K., Welson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chiamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9z7c5
Q9z7c5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
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                                                                                                                                                                                                                                                                                   Local
                                                     111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE001659; AAD18919.1; -. AE002265; AAF38862.1; -. AP002547; BAA98989.1; -.
                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CP1091;
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                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                Similarity
RGAASYNLALGARRANAIKEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTE 186
                                                                                                             DSKEEKQYKSSQVAAFRNITFATDSYTIKGEENLAILTNLVHYMKKNPKATLYIEGHTDE
                                                                                                                                                                      DNDETVKALASKLPSL--VYFDFDSDEIK-PQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNRRAE 160
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                                                                                                                                                                                                                                                                    23.8%; Score 204.5; DB ] 38.7%; Pred. No. 3.2e-11;
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                                                                                                                                                                                                                                                                                             DB 16; Length 192;
                                                                                                                                                                                                                                          46;
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RESULT 28
Q98NA9
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              Kanako T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S.; Takeuchi C., Yamada M., Tabata S.;
                                                                                            STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-MAR-2002 (TrEMBLrel. 20,
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Q92ST9;
01-DEC-2001
01-DEC-2001
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                        Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                        Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capela D., Barloy-Hubber F., Gouzy J., Bothe G., Ampe F., Batut Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
                                                                                                                                                           NCBI_TaxID=381;
                                                                                                                                                                                                                        MLR0220
                                                                                                                                                                                                                                   Hypothetical protein mlr0220
                                                                                                                                                                                                                                                                                                 Q98NA9;
                                                                                                                                                                                                                                                                                                                 Q98NA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591783; CAC41711.1; -
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
    "Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; UNKNOWN 1.
Hypothetical protein; Complete proteome.
SEQUENCE 221 AA; 22852 MW; 3FF7CBA8F69DD396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical transmembrane protein SMc00354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           210 RVEIS 214
                                                                                                                                                                                                                                                                                                                                                                                                                        167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                HTDSTGSASYNQGLSERRAASVANYLASRGVDQRRMSAVGYGLERPIASNATEVGRAQNR 209
                                                                                                                                                                                                                                                                                                                                                                                                                       RAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGVSVTRAGDRII----LNMPSNITFATDRDQVIPAFYSTLDSVAIVLRKFNKTLIDVDG 149
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%;
37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                Last
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                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                      subdivision;
                                                                                                                                                                                                                                                                sequence update)
                                                                                                                                                                                                                                                                                                              216 AA.
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                                                                                                                                                                                 Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 221;
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RESULT
Q8VR19
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                                                                                 RESULT 30
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Q46099;
01-NOV-1996
01-NOV-1996
01-MAR-2002
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ProDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 216 AA; 22401 MW; 6FC9E5B8BAAC404A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesorhizobium loti.";
DNA RES. 7:331-338(2000).
EMBL; AP002994; BABB47852.1; -.
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
Hypothetical 26.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VR19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VR19
                                                                                                                                                                                                                                                                                                           PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa; 1.
                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-2001) to the EMBL/GenBank/DDBJ EMBL; AF448145; AAL46989.1; -. InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                           "A Chemosensory System from Myxococcus xanthus Regulates Developmental Gene Expression Rather than Motility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                       Q46099
                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 249 AA; 26335 MW; 170AF8EFAF632855 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
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                                                                                                                                                                          146 SPVPFGFNESGLSADAQQRLSDLAQCMKT-APGRVTLAGHADERGTEEYNLQLSNRRAAS
                                                                                                                                                    128 VRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                       J.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                        83
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                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt HTDSTGGDQHNFDLSQRRALAVANYLSGQGVDQRRFAVTGFGKTRPIASNATAAGREQNR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTDERGSREYNMSIGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt TGVSVTRSGDQII----LNMPSDITFNVDQDAVKPGFYPVLNSVALVLKKFKQTTVDVFG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVEI 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGVAPLVDNDETVKALASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG
                                                                                                                         VKRYLTDLGVPASQLGTVGYGETRPVNSASSEDAWSENRRVE
                                                                                                                                                                                                      SLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVA
 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. )
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                                                        PRELIMINARY;
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Pred. No. 8.8e-11;
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                                                        165
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    update)
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RESULT 31
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Best Local
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; 047617; AAC35420.1; -
EMBL; JAJ132802; CAA10786.1; -
Interpro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Konkel M.E., Mead D.J., Cieplak W. Jr.; "Cloning, sequencing, and expression of a gene fro jejuni encoding a protein (Omp18) with similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campylobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campylobacter jejuni. Plasmid pUWM97.
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PAL OR CJAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid; Signal. secureNCE 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated lipoproteins.";
Infect. Immun. 64:1850-1853(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96201603; PubMed=8613402;
                                    Chlamydia trachomatis.";
Science 282:754-759(1998).
EMBL; AE001330; AAC68202.1;
                                                                                                                                                                                                  Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae;
                                                                                                                                                                                                                             Peptidoglycan-associated PAL OR CT600.
                                                                                                                                                                                                                                                                                               084605;
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           InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                    Stephens R.S., Kalman S., Lammel C.J., Fa
Mitchell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                  STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                    NCBI_TaxID=813;
ProDom; PD000930;
                                                                             "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                             Davis
                                                                                                                                                                                                                                                                                                                                                                           109 QALGLKRAKAVKEALIAQGVNSDRIAVKSYGETNPVCTEKTKACDAQNRRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                50
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                                                                                             R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     MSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                ISQLNDTL-GKVYFDFDKFNIRPDMQNVVNTNANIFNNEVSGVSITVEGNCDEWGTDEYN
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                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                              N.A.
 Bac_OmpA;
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33.1%;
                                                                                                                                                                                                                                           lipoprotein
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Last annotation update)
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Pred. No. 7.6
                                                                                                                                                                                                                                                                                                              188
                                                                                                           , Fan J.,
L., Zhao
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                                                                                                                        J.
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                                                                                                          , Marathe R., Aravind Q., Koonin E.V.,
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RESULT 33
Q9XCZ6
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Q9PJE0
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                 Q9XCZ6
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_Ompa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-MOPN / NIGG;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002355; AAF39684.1; TIGR; TC0889; -.
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                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001145; Bac_OmpA
                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                            118 VRHLRKSPKTTLYIEGHTDERGAAAYNLALGARRANAVKQYLIKQGIASDRLFTISYGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 HPVHPGHNELAWQQNRRTE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 GVAPLVDNDETVKALASKLPSL-------VYFDFDSDEIKPQ-AAAILDEQ
                                                                                                                                                                                                                                                                         48;
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                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                       AQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEE
                                                                                                                                                                                                   GFVPFYSDEEIQQAFVEDFDSKEEQLYKTSAQSTSFRNITFATDSYSIKGEDNLTILASL 117
                                                                                                                   RPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                        HPVHSGHNELAWQQNRRTE 196
                                                                                                                                                                                                                                        GVAPLVDNDETVKALASKLPSL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFVPFYSDEEIQQAFVEDFDSKEEQLYKTSAQSTSFRNITFATDSYSIKGEDNLTILASL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                              202 AA;
               PRELIMINARY;
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                           23208 MW; 02F2F13F6CDF6901 CRC64;
                                                                                                                                                                                                                                                                                    22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%; Score 196.5; 35.3%; Pred. No. 1.7
                                                                                                                                                                                                                                                                  19; Mismatches
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                                                                                                                                                                                                                                                                                    Score 196.5; DB : Pred. No. 1.9e-10
              PRT;
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              A
                                                                                                                                                                                                                                                                                             DB 16; Length 202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels 17;
                                                                                                                                                                                                                                                               55; Indels
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    Q9XCZ

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InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
PrODom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; UNKNOWN_1.
                                                                             fixing Pseudomonas stutzeri.";
Syst. Appl. Microbiol. 22:215-224(1999).
EMBL; AF117975; AAD39370.1; -
                                                                                                                                                                                                                                                                                                                Q9XCZ3;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 1)
                                                                                                                                                                                                                                                                                                     Outer membrane protein OprF
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SEQUENCE
                                                                                                                                         Vanderleyden J.;
                                                                                                                                                    Vermeiren H., Willems A., Schoofs G.,
                                                                                                                                                                    MEDLINE=99319345;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                          Pseudomonas stutzeri ZoBell.
                                                                                                                                                                                                                                                                                                                                                                                   Q9XCZ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001145; Bac_OmpA.
Pfam; PF00651; OmpA; I.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; UNKNOWN_1.
NON TEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fixing Pseudomonas stutzeri.";
Syst. Appl. Microbiol. 22:215-224(1999).
EMBL; AF117972; AAD39367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09XCZ6;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein OprF (Fragment).
                                                                                                                                                                                                                                 NCBI_TaxID=96564;
                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                      The rice inoculant strain Alcaligenes faecalis Al5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=LMG 10652;
MEDLINE=99319345; PubMed=10390872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vermeiren H., Willems A., Schoofs G., de Mot R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=91504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ERGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 E 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 APIVDNEPEPAPEVVRVELDVKFDFDKSRVREESYSDIKNLADFMQQYPQTTTVVEGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 APLVDNDETVKALASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                         Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 AA;
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                    PubMed=10390872;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.5%; Score 193.5; 35.5%; Pred. No. 7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Pseudomonadaceae;
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Mismatches

Indels Length 321;

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Gaps

259

/e-10; DB 2; 56;

Keijers V., Hai W.,

(Fragment).

de Mot R., Keijers V., Hai W.,

is a nitrogen-

Last sequence update)
Last annotation update)

Created)

PRT;

321 AA.

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                                                            RESULT 36
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Best Local Similarity
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SEQUENCE
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein OprF (Fragment).
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PRODOM; PD000930; Bac_Cmph, UNKNOWN_1.
PROSITE; PS01068; OMPA; UNKNOWN_1.
323 323 427 Mul: 14F
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Vermeiren H., Willems A., Schoofs G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=DSM 4066;
MEDLINE=99319345;
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InterPro; IPR001035; MotY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fixing Pseudomonas stutzeri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The rice inoculant strain Alcaligenes faecalis Al5 is a nitrogen-
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                                                                                                                                                                                                                                                                                        FMQQYPQTTTVVEGHTDSVGTDQYNQRLSERRAEAVRNVLVNEYGVQGNRVNSVGYGESR 304
                                                                                                                                                                                                                                                                                                                                                     FLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK-GINQASVEITSFGEER 151
                                                                                                                                                                                                                                                                                                                                                                                                                       VAPVEPTP----EPAPAPIVDTEPEPAPEVVRVELDVKFDFDKSRVREESYSDIKNLAD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQ 92
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                                                                                                                                                             PVADNSTEEGRQINRRVE 322
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321 AA;
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323 AA;
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   PRELIMINARY;
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34.1%;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14EEF230B4CDA559 CRC64;
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   261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
..2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 323;
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      Q8UBX6
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MEDLINE-21608550: PubMed=11743193;

MEDLINE-21608550: PubMed=11743193;

MOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa; PROSITE; PS01068; OMPA; 1.
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Pfam; PF00691; OmpA; 1.
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 LQNASAQRAQARLDARTAQLDKLRSQL----NAKQTSRGTMVTF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 AA;
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31.7%;
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16, Last sequence update)
18, Last annotation updat
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Last annotation update)
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"L. Nature 415.497-502(2002).

"RemBL; AL646080; CAD17912.1; -.

"R EMBL; AL646080; CAD17912.1; -.

"R FINTS; PR01021; OmpA; 1.

"R PRINTS; PR01021; OMPADOMAIN.

"ProDom; PD000930; Bac_OmpA; 1.
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            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid megaplasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
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Complete proteome.
277 AA; 28898 M
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      28898 MW;
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Pred. No. 1.1e-09;
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MEDLINE-20020109; PubMed-11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009519; AAL51967.1; .
InterPro; IPRO1145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_Ompa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00691; OmpA; 1.
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                                                                     137 INQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                  131 DQVKSQFYPTLNSVAIVLRKFDKTLVDVYGFTDSTGSASYNQALSQRRAASVASYLDSQG
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                                                                                                                                                                                                                                                                 4 HIQIAAAAAALSVLTFMTGC-ANKSTSQVMV-----APNAPTGYTGVIYTG-----
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                                                                                                                                                                                                                                                                                                                      Similarity
                                        IDPRRFAVIGYGASQPIASNATPEGRAQNRRVEI 224
                                                                                                                                 DEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKG 136
                                                                                                                                                                                                                                                                                                                                                             232 AA; 24422 MW; 528DE7B4367E73FF CRC64;
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27.1%; Pred. No. 1.6
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31.3%;
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20, Last sequence update)
21, Last annotation update)
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Pred. No. 1.5e-09;
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Search completed: July Job time : 63 secs
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Syst. Appl. Microbiol. 22:215-224(1999).

Rembl; AF117971; AAD39366.1; -.
Rembl; AF117971; AAD39366.1; -.
Rembl; AF117971; AAD39366.1; -.
Rembl; AF117971; AAD39366.1; -.
Remonas; PR001035; Motv.
Remonas; PR001035; Motv.
Remonas; PR01023; NAPFLGMOTY.
Remonas; PR01021; OMPADOMAIN.
Remonas; PR01021; OMPADOMAIN.
Remonas; PR01021; OMPADOMAIN.
Remonas; PR01068; OMPA, UNKNOWN_1.
Remonas; PS01068; OMPA, UNKNOWN_1.
Remonas; PS01068; OMPA, UNKNOWN_1.
Remonas; PS01068; OMPA, UNKNOWN_1.
Remonas; PS01068; OMPA, UNKNOWN_1.
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STRAIN=LMG 111997;
MEDLINE=99319345; PubMed=10390872;
Vermeiren H., Willems A., Schoofs G., de Mot R., Keijers V., Hai W., Vanderleyden J.;
Vanderleyden J.;
"The rice inoculant strain Alcaligenes faecalis Al5 is a nitrogen."
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Ol-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein OprF (Fragment).
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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NCBI_TaxID=316;
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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US-08-469-260A-605
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US-08-475-989-39
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US-08-912-3
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Sequence 28, Appli
Sequence 29, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 47, Appli
Sequence 57, Appli
Sequence 17, Appli
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5173294-2
;Patent No. 5173294
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NUMBER OF SEQUENCES: 3
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: M. Paul Barker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 14-DEC-19
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/92,948
FILING DATE: 08-0CT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 932,872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MURPHY, TIMOTHY F.; APICELLA, MICHAEL A. TITLE OF INVENTION: DNA PROBE FOR THE IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                    REFERENCE/DOCKET NUMBER:
                                      REGISTRATION NUMBER:
                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO: 2
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                            'AGENT IN ...
M. Paul Barker
M. Paul Barker
32,013
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                                                                                                                                                                           14-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic Hybrid Protein OprF-OprI
Derived From Pseudomonas aeruginosa Membrane Proteins
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                                                                                                                                                                                           US/08/572,447C
                05552.1395-00000
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; MOLECULE TYPE:
US-09-267-747-13
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                                                                                                         TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                            REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 14-DEC-1995
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
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                                                      TYPE:
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FILING DATE: 16-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                     LENGTH:
                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                   TOPOLOGY:
                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                    NAME:
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                                                                   214 amino acids
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202) 408-4400
                                                                                                                                             (202) 408-4000
                protein
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                                                                                                                                                                               05552.1395-00000
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US/0
FILING DATE: 07-MAR-1994
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: unl TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Harrington, James J
REFERENCE/DOCKET NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                            235 QAQATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADA 294
                                                                                                                                                                                             184 INPNTAIHYNPXIGSINAGISYRFGQGAAP-----VKTFSLNLD--VTFAFGKANLKP 234
                                                                                             142 VEIISFGEERPIAFGTNEEAWSQ-----NRRAELS 171
                                                             295 ISATGYGKANPVTGATXDQVWGRWALIATLAPDRRVEIA 333
                                                                                                                                                          82 QAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQAS 141
                                                                                                                                                                                                                               33 VAPNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKP
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                                                                                                                                                                                                                                                                                                                                                                                              unknown
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Purified No. 5770213typable Haemophilus
influenzae P5 Protein as a Vaccine for No. 5770213typable
Haemophilus Influenzae Strain
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                                                                                                                                                                                                                                                                       27;
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RESULT 6
US-09-267-747-11
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                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Knapp, Bernhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELETAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 161 amino acids
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APPLICANT: Domdey, H
TITLE OF INVENTION:
TITLE OF INVENTION:
                           APPLICANT: Knapp, Bernhard
APPLICANT: Hungerer, Klaus-Dieter
APPLICANT: Broker, Michael
APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
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APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                     NUMBER OF SEQUENCES:
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ADDRESSEE: Finnegan, Henderson, Farabow,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATE: Patentin Release #1.0,
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STREET: 1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: M. Paul Barker REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 14-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                               130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
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Broker, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.9%; Score 171.5; DB 2 37.6%; Pred. No. 7.3e-13;
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Derived From Pseudomonas aeruginosa Membrane Proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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Best Local 9
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APPLICANT: Knapp, Bernhard
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
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APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                    APPLICANT: Domdey, Horst TITLE OF INVENTION: Immur TITLE OF INVENTION: Deriv NUMBER OF SEQUENCES: 15
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32,013
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                                                           ZIP: 20005-3315
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                                                                                                                                                ADDRESSEE:
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                                                                        COUNTRY:
                                                                                                                                                                ADDRESSEE: Finnegan, Henderson, Farabow,
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                                                                                                            Washington
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amino acid
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                                                                                                                        3: Dunner
1300 I Street, N.W.,
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                                                                          USA
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                                                                                                                                                                                                      Derived From Pseudomonas aeruginosa Membrane Proteins
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37.6%; Pred. No. 7.3e-13;
tive 15; Mismatches 47
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                                                                                                                               Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Knapp, Bernhard
APPLICANT: Hungerer, Klaus-Dieter
APPLICANT: Broker, Michael
APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Dondey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
NUMBER OF SEQUENCES: 15
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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ATTORNEY/AGENT INFORMATION
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 16-DEC
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                APPLICATION NUMBER: US/0 FILING DATE: 14-DEC-1995 APPLICATION NUMBER: EP 9 FILING DATE: 16-DEC-1994
                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 I St
CITY: Washington
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                                                                                                                    CLASSIFICATION:
                                                                                                                                           FILING DATE
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20005-3315
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                                          EP 94120023.0
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                                                                           Matches
                                                                                                            Query Match
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                                                                                                                                                                                                                                                        TELEFAX: (216) 241-0816 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
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REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Cleveland
                                                                         Local Similarity tes 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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199 PNTAINYNPWIGCINAGISYRFGQGEAPVVAAPEMVSKTFS-LNSDVTFAFGKANLKPQA 257
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                                  35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
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Suite 1800 800 Superior Avenue
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                                                                                         19.2%;
29.9%;
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                                                                                       Score 165.5; DB 1
Pred. No. 1.3e-11;
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                                                                                          RESULT 11
US-08-836-500A-2
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                Sequence 2, Application US/08836500A
Patent No. 6197929
GENERAL INFORMATION:
APPLICANT: Binz, Hans
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
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APPLICANT:
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Baussant, Thierry
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 165.5; DB 3; Pred. No. 1.3e-11;
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RESULT 12
US-08-469-260A-605
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Best Local S
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
                                                                APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C,
TITLE OF INVENTION: REAGENTS AND METHODS
                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Katz, Martin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 312-616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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STREET: 4700
                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   124 RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE-----EAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                     266 RAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 LKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER 123
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: Illinois
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                                                                                                                                                                         GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
     100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 amino acids
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                                                                                                                                                       ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                            JOHN N. SIMONS
TAMI J. PILOT-MATIAS
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   ABBOTT LABORATORIES

0 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312-616-5400
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Effect, Immunogenic Complex Containing It, Process
Their Preparation, Nucleotide Sequence and Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 136.5; DB 4; Length 335; Pred. No. 3.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                      METHODS FOR THEIR USE
                   D377/AP6D
                                                                                      NON-D, NON-E HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
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COUNTRY:
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US-08-469-260A-83
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                                                                                                                                                                                                                                                                                                                                      Sequence 83,
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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                               CORRESPONDENCE ADDRESS:
                                                                                              TITLE OF INVENTION:
                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                               NUMBER OF SEQUENCES:
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               CITY:
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REFERENCE/DOCKET NUMBER: 5527.PC.01
STATE:
                               STREET:
                                             ADDRESSEE: ABBOTT LABORATORIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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            ABBOTT PARK
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                                                                                              INVENTION: REAGENTS AND METHODS
                                                                                                                         SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                   Application US/08469260A
                            100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507 amino acids
                                                                                                                                                                                                                                  GEORGE J. DAWSON
GEORGE G. SCHLAUI
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                                                                                                                                                                                                                                                                JOHN N. SIMONS
TAMI J. PILOT-MATIAS
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                                                                                                                NON-A, NON-B.
                                                                                716
                                                                                                                                                                                                                                    SCHLAUDER
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                                               D377/AP6D
                                                                                                                NON-C, NON-D,
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                                                                                                FOR THEIR USE
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                                                                                                                NON-E HEPATITIS
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Gaps

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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 83:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                          APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
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LENGTH: 1422 amino aci
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  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                         COUNTRY: USA
ZIP: 60064-3500
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                                                                                                  CITY: ABBOTT PARK
                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                             GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                  E: ABBOTT LABORATORIES D377/AP6D 100 ABBOTT PARK ROAD
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TAMI J. PILOT-MATIAS
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Floppy disk
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RESULT 15
US-08-475-989-41
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                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5679352

Patent No. 5679352

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KAUDIL, Ali
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: Synthetic Haemophilus Influenzae
TITLE OF INVENTION: Conjugate Vaccine
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41, Approx. 5679352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
EILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   ZIP: M5G 1R7
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TELEPHONE: 708-938-2623
                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      STREET: Suite
CITY: Toronto
                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/469,260A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1566 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT------VAPVVDEEEIVEEC 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 RRA--VAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 10.2%; Score 87.5; DB Similarity 28.4%; Pred. No. 0.92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                   Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08475989
                                                                                                                                                                                                                                                                                                               E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2864 amino acids
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SYSTEM: PC-DOS/MS-DOS
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33,207
MRR: 5527.PC.01
                    US 08/256,839
                                                                                                  US/08/475,989
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RESULT 16
US-08-475-985-41
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APPLICANT: CHONG, Pele
APPLICANT: KANDIL, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: |
FILING DATE: 03-FEB-1
                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,839
FILING DATE: 03-FEB-1993
                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Synthetic Haemophilus Influenzae
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                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 9 FILING DATE: 03-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                FILING DATE:
                            APPLICATION NUMBER: GB 9202219.3
                                                                                                                                    CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIA, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                              Floppy disk
            03-FEB-1992
                                                                                 03-FEB-1993
                                                                                                                                                    03-FEB-1993
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53.6%;
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                                                                                                 PCT/CA93/00041
                                                                                                                                                                                                                                           US/08/475,985
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Pred. No. 0.0021;
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                                                                                                          TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6018019
GENERAL INFORMATION:
                               Query Match
    Matches
                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                            REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-373 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Synthetic Haemophilus Influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 ISFGEERPIAFGTNEEAWSQNRRAELSY 172
    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VSYGEEKPAVLGHDEAAYSKNRRAVLAY 30
                                                                                                                                                                                                                                                                                                                                                                                                              RY: Canada
M5G 1R7
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08256839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHONG, Pele
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KANDIL, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                  9.8%;
53.6%;
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53.6%;
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7; Mismatches
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Pred. No. 0.0021;
                 Score 84; DB 3;
Pred. No. 0.0021;
                  0.0021;
                                Length 30;
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    0,:
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   Gaps
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145 ISFGEERPIAFGTNEEAWSQNRRAELSY 172

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VSYGEEKPAVLGHDEAAYSKNRRAVLAY 30

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; SOFTWARE: FastSEQ for SEQ ID NO 177; LENGTH: 964; TYDE: PRT; ORGANISM: Chlamydia US-09-556-877-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
US-09-620-412C-177
; Sequence 177, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.46907
; FILE REFERENCE: 210121.46907
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US-09-556-877-177
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 177
LENGTH: 964
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Best Local Similarity
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APPLICANT: Maisonneuve, Jeff
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
FILE REFERENCE: 210121.469C5
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CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
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                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Chlamydia
                                                                                                                                                                                                 Match 9.4%;
Local Similarity 23.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 334
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Skeiky, Yasir
Fling, Steve
KGGAIYIDGTSN-----SKISADRHAIIFNENIVTNVTNANGTSTSANPP-----RRNA 383
                                                                                       ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 334
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23.6%;
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s; Pred. No. 1;
23; Mismatches
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Pred. No. 1;
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; Sequence 191, Application US/09620412C
; Patent No. 6448234
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US-09-556-877-191
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SOFTWARE: FASTSEQ FOR WARE: SEQ ID NO 191
SEQ ID NO 191
LENGTH: 977
TYPE: PRT
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SEQ ID NO 191
LENGTH: 977
TYPE: PRT
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Best Local S
Matches 39
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Patent No. 64329
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                                                                                         Matches
                                                                                                         Query Match
Best Local :
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
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CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
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APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
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290 ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 347
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                                           8 AAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDET--VKALASK 65
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                                                                                                            Similarity
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                                                                                                       9.4%; Score 81; DB 4; Length 977; 23.6%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                         Windows Version 3.0/4.0
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                                                                                     23;
                                                                                         Mismatches
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US-08-475-989-39
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                                                                                                              Best Local Similarity Matches 15; Conserv
                                                                                                                                                 Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                       TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PC
FILING DATE: 03-FEB-19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRETY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/256,839
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                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/475,989 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada ZIP: M5G 1R7
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                                         RGTPEYNIALGQRRADAVKGYLAG 24
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                                                                                                                                                                                                                                                        24 amino acids
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Suite 701, 330 University Avenue
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                                                                                                                Conservative
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KLEIN, Michel
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                                                                                                            5; Mismatches
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                                                                                                                             Score 79; DB 1;
Pred. No. 0.0059;
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US-08-475-985-39
                                                                 Sequence 39, Applicat:
Patent No. 6018019
GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                       Matches
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                APPLICANT:
APPLICANT:
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LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: PCT/CA93/00041
APPLICANT:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/256,839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Synthetic Haemophilus Influenzae TITLE OF INVENTION: Conjugate Vaccine NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KANDIL, Ali
APPLICANT: SIA, Charles
APPLICANT: KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Sur
TTY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-506 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 0: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 03-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 07-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                 111 RGSREYNMSLGERRAVAVRNYLLG 134
                                                                                                                                                                                              1 RGTPEYNIALGQRRADAVKGYLAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9, Application US/08475985
5972349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEWART, MICHAEL
                                                                                                      Application US/08256839
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                KANDIL, Ali
SIA, Charles
                                                      CHONG, Pele
                                                                                                                                                                                                                                                                       Conservative
KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (416) 595-1155
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                                                                                                                                                                                                                                                                                  9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB 9202219.3
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                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                      Score 79; DB 2; Pred. No. 0.0059;
                                                                                                                                                                                                                                                                                                      Length 24;
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Gaps

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RESULT 25
5206163-3
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                                                                                                                                                                                            Query Match
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ZIP: M5G 1R/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OVETEM: PC-DOS/MS-DOS
COMPUTER: COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/550,816
FILING DATE: 06-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: RENARD, ANDRE; DINA, DINO; MARTIAL, JOSEPH TITLE OF INVENTION: DNA ENCODING BOVINE DIARRHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
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NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,
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                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 331,037
FILING DATE: 29-MAR-1989
APPLICATION NUMBER: 752,981
FILING DATE: 08-JUL-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-373 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/256,839 FILING DATE:
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Local Similarity 62.5%;
                                                                                                                                                                           Local
                                                                                                                                                                                                                                                         LENGTH: 2616
1729 TLADE---IHSRDERPFYLYLGSRSSMSNRAKTARNINCTQKRPQEIRDLMAQGRMLYVA 1785
                                                                              1675 TSEVGI---TLVGRAALMTTGITPVVEKTE---PNADGSPSSIKIGLDEGCYDGPRPQDH 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 RGSREYNMSLGERRAVAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                     28 TSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDS---DEIKPQAA 84
                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424
                                                                                                                                                      9.2%; Score 79; DB
21.8%; Pred. No. 8.5;
7ative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic Haemophilus Influenzae
Conjugate Vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
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                                                                                                                                                                                                DB 6; Length 2616;
                                                                                                                                                             68; Indels 40;
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RESULT 26
US-09-074-579-5
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                                                                                                         RESULT 27
US-09-388-774-5
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                                                                     ; Sequence 5, Application US/09388774 ; Patent No. 6228991
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                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                      Query Match 8.8%; Score 76; DB 3; Length 885; Best Local Similarity 25.5%; Pred. No. 3.7;
GENERAL INFORMATION:
APPLICANT: Hillman
APPLICANT: Guegles
APPLICANT: Patters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Perfect 6.1/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/074,579
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                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: GENEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650-65-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                              177 HFEIEVDIFEPQGISMLDAEASFITNDLLGSALTKSFSGKKGHVSFKPSLDQQRS 231
                                                                                                                                                                                                                 71 YFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                         Conservative
                 Hillman, Jennifer L.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                     GENEBANK
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                                                                                                                                                                                                                                                         16; Mismatches
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TITLE OF INVENTION:

Patterson, Chandra FENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE

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25;

Gaps

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RESULT 28
US-08-762-106-9
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                                                                                                                                                                                                                                                                                                                                   Patent No. 5948677
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08762106 Patent No. 5948677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                           APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
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LIBRARY: GENEB
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LENGTH: 885 amino acid
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REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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NAME: Cerrone, michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
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APPLICATION NUMBER: US/09/388,774
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                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                         APPLICATION NUMBER:
                                                                                                                                                                  COUNTRY:
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            FILING DATE:
                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                    92037
                                                                                                                                                                                 La Jolla
California
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202 Coast Blvd., Suite 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc
                                                                                                            Floppy disk
            09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 76; DB 4
25.5%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOS
                     US/08/762,106
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US-09-320-774-9
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US-09-320-774-9
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                                                                                                                     INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
              MOLECULE TYPE: FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Brotman, Harris F.
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
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                                                             TYPE: amino acid
                                                                                                                                                                      NAME: Brotman, Harris
REGISTRATION NUMBER: (
                                                  TOPOLOGY:
                                                                                 LENGTH:
                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/320,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 PTGYTGVIYTGVAPLVDNDETVKALASKLPSLV----YFDFDSD------EIK 80
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)GY: linear
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STATE: STREET: Matches Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1312
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CARBOHYD LOCATION: 432..434 OTHER INFORMATION:
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                                                                                                                           NAME/KEY: CARBOHYD
LOCATION: 1151..1153
OTHER INFORMATION: potential
                                                                                                                                                                                                                                       NAME/KEY: CARBOHYD LOCATION: 910..912
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                                         LOCATION: 1226..1228
OTHER INFORMATION: potential
                                                                                       NAME/KEY: CARBOHYD
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OTHER INFORMATION:
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NAME/KEY: PHOSPHORYLATION
                           FEATURE:
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859..861
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NAME/KEY: PHOSPHORYLATION LOCATION: 808..811 NAME/KEY: PHOSPHORYLATION LOCATION: 663..666 LOCATION: 102..105
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION LOCATION: 17..19
OTHER INFORMATION: potential LOCATION: 808..811
OTHER INFORMATION: potential OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION LOCATION: 41..43 OTHER INFORMATION: potential OTHER INFORMATION: potential FEATURE FEATURE: LOCATION: 31..33
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION NAME/KEY: PHOSPHORYLATION LOCATION: 531..533 LOCATION: 507..509
OTHER INFORMATION: potential LOCATION: 471..473
OTHER INFORMATION: potential LOCATION: 216..218
OTHER INFORMATION: potential OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION FEATURE: OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION LOCATION: 100..102 NAME/KEY: PHOSPHORYLATION EATURE: LOCATION: 885. NAME/KEY: PHOSPHORYLATION NAME/KEY: PHOSPHORYLATION NAME/KEY: PHOSPHORYLATION LOCATION: 812..814 LOCATION: 801..803
OTHER INFORMATION: potential LOCATION: 656..658
OTHER INFORMATION: potential LOCATION: 591..593 OTHER INFORMATION: potential OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION LOCATION: 815..817
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION FEATURE OTHER INFORMATION: potential FEATURE: NAME/KEY: PHOSPHORYLATION FEATURE: NAME/KEY: PHOSPHORYLATION FEATURE: NAME/KEY: PHOSPHORYLATION LOCATION: 876..878 FEATURE NAME/KEY: PHOSPHORYLATION 656..658

OTHER INFORMATION: potential

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LOCATION: 295..298
OTHER INFORMATION: potential
                                                                    NAME/KEY: PHOSPHORYLATION LOCATION: 276..279
OTHER INFORMATION: potential
                                      NAME/KEY: PHOSPHORYLATION
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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NAME/KEY: PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: potential
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OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AME/KEY: PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EATURE:
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OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PHOSPHORYLATION OCATION: 1129..1131
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US-08-790-912-3
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                                                                                      Matches
                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                           NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 7600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,939
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Plaut, Andrew G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
NUMBER OF SEQUENCES: 10
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                                                                                                      Local
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CITY: Philadelphia
STATE: Pennsylvani
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1195 LKYQTDFAN-----LPEYNLGNTGLLYTPNQFLYDRDSIVKEV---LPELQKLDYQS 1243
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                                   17 LTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 YNMSLGERRAVAVRNYLLGKGINQASVEIISFGE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 DEIKP-----QAAAILDEQAQFLTTNQ------TARVLV----AGHTDERGSRE 115
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                                                                                                  h 8.5%; Score 73; DB Similarity 23.6%; Pred. No. 29;
                                                                                                                                                                                                                                    amino acid
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                                                                                  Conservative
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22.1%; Pred. No. 16;
ative 22; Mismatches
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                                                                            19; Mismatches
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                                                                                                                  DB 2; Length 1964;
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                                                                            57; Indels
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US-08-790-912-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 7600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                   ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 -----SREYNMSLGERRAVAVRNYLL-----GKGINQASVEIISFGE 149
1376 IKNNKEALLLGLTYLERWYNFNYGQ---VNVKDLVMYHPDFFGKGNTSPLDTLIELGK 1430
                                                                                1317 DAIR-KTLGISPEVKLTELYLEDQFSKTKQNLGDSLKKLLSADAGLASDNSVTRGYLVDK 1375
                                                                                                                                                                1268 LKYQTDFAN-----LPEYNLGNTGLLYTPNQFLYDRDSIVKEV---LPELQKLDYQS 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 DEIKPQAAAILDE------QAQFLTTNQTA------RVLVAGHTDERG----- 112
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                                                                                                                                                                                                       17 LTFMTGCANKSTSOVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDS 76
                                                                                                                                                                                                                                                  42; Conservative
                                                                                                                       77 DEIKPQAAAILDE------QAQFLTTNQTA------RVLVAGHTDERG----- 112
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                                                                                                                                                                                                                                                                                                                                                                                                                2052 amino acids
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                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                 8.5%; Score 73;
23.6%; Pred. No.
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                                           -- SREYNMSLGERRAVAVRNYLL-----GKGINQASVEIISFGE 149
                                                                                                                                                                                                                                                  19; Mismatches
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RESULT 33 US-08-960-756-2

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                                                                                             Sequence 2, Application US/07920281C patent No. 5739026 GENERAL INFORMATION:
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APPLICANT: WAYNE,
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
            APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based on
TITLE OF INVENTION: Alphaviruses
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                     147 ERLILLRELMADSGLIFVHIDEKYGFEVKLILDEVFGRRNFV---NHIARIASNPKNFSR 203
                                                                                                                                                                                                                     204 KAFGSQKDMILVYSKTRDYVWNES 227
                                                                                                                                                                                                                                                     145 ISFGEERPIAF --- GTNEEAWSQN 165
                                                                                                                                                                                                                                                                                                                                                    87 PGGYAGKVQLVYIDPPYGTGQQFLVGGDETDRVATVSQPKNGQLGYDDTLDGPQFVEFLR 146
                                                                                                                                                                                                                                                                                                                                                                                      38 PTGYTG---VIY-----TGVAPLVDNDETVKALASKLPSLYYFDFDSDEIKPQAAAILD 88
                                                                                                                                                                                                                                                                                                                    89 EQAQFLTTNQTARVLVAGHTDERGSREYNMSL----GERRAVAVRNYLLGKGINQASVEI 144
                                                                                                                                                                                                                                                                                                                                                                                                                        34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New England Biolabs, Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72.5; DB 2; pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEB-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 413;
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US-08-466-277-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08466277 Patent No. 6190666
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
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                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 13-AUGCLASSIFICATION: 435
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                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. Box 7.
CITY: Falls Church
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                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA Expression Systems Based on
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Garoff, Henrik
Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1799 SGITFGDFDDVLRLGRAGAYIFSSDTG----SGHLQQKSVRQHNLQCAQLDAV 1847
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                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1756 ASRAAERPVPAPRKPT------PAPRT-----AFRNKLP-LTFGDFDEHEVDALA 1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                              APPLICATION NUMBER: US/08/466,277
FILLING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: 07/920,281 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                     CITY: Falls Church
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
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                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                   STATE: Virginia
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O. Box 747
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23.0%; Pred. No. 46;
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                                                                                                                                                                                                                                                                                                                                                                               Alphaviruses
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: FAIRWEATHER, Neil Fraser
APPLICANT: MAKOFF, Andrew Joseph
TITLE OF INVENTION: Expression of tetanus toxin fragment C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                          APPLICATION NUMBER: GB 80 FILING DATE: 20 June 1980 ATTORNEY/AGENT INFORMATION: NAME: Mary J. Wilson
                                                                                                                                                                                                                                                           FILING DATE: 29-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/110 FILING DATE: 23-AUG-1993 1991 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                  TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
                                                TELEPHONE:
                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 8.4%; Score /..., Similarity 23.0%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2431 amino acids
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1100 No. 5443966th Glebe Road
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                                                      816-4000
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US-08-306-871-47
                                                             US-08-306-871-47
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           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                           TELEFAX: (716) 849-034
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/129,719 FILING DATE: September 29, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                              FEATURE:
                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS/ Microsol SOFTWARE: Wordperfect for Windows
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/306,871 FILING DATE: 20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Buffalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                           STRAIN:
                                                                                                                            ORGANISM:
                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 VDNDETVKALASKLPSLVYFDFDSDEIK------PQAAAI--LDEQAQFLTTNQ 98
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19;
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                                                                                                                                                                                                                                                                                                                           Nelson, M. Bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDNEEDIDVILKK-SNILNLDINNDNISDISGSNSSRITYPDAQLVPGINGKAIHLVNNE 66
                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 amino acids
                                                                                                               25240
                                                                                                                                                                                          59 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Timothy F. Murphy VENTION: Vaccine For Branhamella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
Conservative
                                                                             CD amino acid positions 332-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                             linear
                                                                                                                            Branhamella catarrhalis
                                                                                                                                                                                                                                                           (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; but
20.9%; Pred
25;
                                                                                                                                                                                                                                            849-0349
             8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MS-DOS/ Microsoft Windows 3.1 fect for Windows 5.1
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                                                                                                                                                                                                                                                                                                         35,300
                                                                                                                                                                                                                                47:
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8;
                                                                                                                                                                                                                                                                                             11520.0053
             Score 70; DB 1
Pred. No. 0.29;
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 Mismatches
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                             DB 1; Length 59
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 26;
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4;
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US-08-569-959-47
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US-08-569-959-47
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                                                                                                                                                                                                                                                                                                         QΨ
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                                                                                                                                                                                                                        RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 47, Application US/08569959
Patent No. 5725862
                                                                                                                                                                     Sequence 2, Application US/08854585 Patent No. 6114140
                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                               GENERAL INFORMATION: Tonks, Nicholas K. and Stman, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1 SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: September 2
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 59 residues
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STREET: STREET: Chicago
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                      TITLE OF INVENTION:
                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/569,959
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                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                          100 ARVLVAGHTDE---RGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISFGEERP 152
                                                                                                                                                                                                                                                                                                                                               19;
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                                                                                                                                                                                                                                                                          3 ATATIEGHASRDSARSSARYNQRLSEARANAVKSMLSNEFGIAPNRLNAVGYGFDRP 59
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                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25240
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                                                  233 South Wacker Drive, Suite 6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (716)
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                                                                                                                                                                                                                                                                                                                                                                                                                                CD amino acid positions 332-390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (716)
                                                                    Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: U.S. 08
September 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         849-0349
                                                                                                                                                                                                                                                                                                                                                         8.1%;
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                                                                                                                     Density Enhanced Protein Tyrosine Phosphatase
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Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                               Mismatches
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COMPUTER READABLE FORM:

COUNTRY:

United States of America

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PCT-US95-05512-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICANT: Tooks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
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                                                                       NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                 STREET: 233 Sout
CITY: Chicago
STATE: Illinois
                                    TELEPHONE:
                                                                                                                                                         FILING DATE:
                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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Local Similarity 21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 ATSLTLIWKVSDNES---SSNYTYKIHVAGETDSS----NLNVSEPRAV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 SGQQSRDTEVLLVGLEPGTRYNATVYSQAANGTEGQP--QAIEFRTNAIQVFDVTAVNIS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 PQAAAIL----DEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 TGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIK 80
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                                                                                                                                                                                                                                                                                                                60606
                                                                                                                                                                                                                                                                                                                                                                                   233 South Wacker Drive, Suite 6300
                  : 312-474-6300
312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                         27866/31954
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Pred. No. 49;
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Search completed: July 6, 2003, 14:08:12 Job time: 39 secs
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                                                                                                                                                                                             Вþ
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                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein PCT-US95-05512-2
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LENGTH: 1337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                             379 ATSLTLIWKVSDNES---SSNYTYKIHVAGETDSS-----NLNVSEPRAV 420
                                                                                                                                                                                   321 SGQQSRDTEVLLVGLEPGTRYNATVYSQAANGTEGQP--QAIEFRTNAIQVFDVTAVNIS 378
                                                                                                                      81 PQAAAIL----DEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                21 TGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIK 80
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                                                                                                                                                                                                                                                                                 46; Indels 14;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                           Pred. No.
   re greater than or equal to the score of the result bein is derived by analysis of the total score distribution.
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seq length:
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                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                             Published_Applications_Aa:*

1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
4: /cgn2_6/ptodata/2/pubpaa/U
5: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
9: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
13: /cgn2_6/ptodata/2/pubpaa/U
14: /cgn2_6/ptodata/2/pubpaa/U
                                                                                                                                                                                                                                                                                                            is the number of results predicted by chance to have a ater than or equal to the score of the result being printed.
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Gapop 10.0 ,
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: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen
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US-10-1203-942-9

US-10-156-761-10782

US-09-98-279-26

US-09-998-279-24

US-09-98-279-24

US-08-424-5508-605

US-08-424-5508-394

US-09-742-659-6

US-09-742-659-6

US-09-742-659-6

US-09-846-132-177

US-09-841-132-191

US-10-156-761-3758

US-09-815-724-2-14076
Sequence 2, Appli
Sequence 10782, A
Sequence 10782, A
Sequence 26, Appli
Sequence 24, Appl
Sequence 24, Appl
Sequence 66, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 6, Appli
Sequence 21, Appl
Sequence 27, Appl
Sequence 177, App
Sequence 191, App
Sequence 191, App
Sequence 13758, A
Sequence 13758, A
Sequence 14076, A
                                                                                                                                                                                                                                     Description
    \begin{array}{c} 1855 \\ 1857 \\ 1944 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 1946 \\ 19
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10 US-09-815-242-5697
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10 US-09-815-242-5697
10 US-09-815-242-10417
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10 US-09-815-242-568
10 US-09-815-242-568
10 US-09-815-242-13680
10 US-09-815-242-13680
10 US-09-97-182-133
10 US-09-9815-242-1344
10 US-09-815-242-1344
10 US-09-
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Sequence 5, Appli Sequence 10510, A Sequence 10417, Appli Sequence 10417, Appli Sequence 10417, Appli Sequence 13680, Appli Sequence 133, Appli Sequence 133, Appli Sequence 141, Appli Sequence 133, Appli Sequence 141, Appli Sequence 13113, Appli Sequence 13114, Appli Sequence 10029, Appli Sequence 10029, Appli Sequence 10029, Appli Sequence 10029, Appli Sequence 13144, Appli Sequence 13146, Appli Sequence 23, Appli Sequence 13146, Appli Sequence 21, Appli Sequence 23, Appli Sequence 23, Appli Sequence 21, Appl

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US-10-203-942-9
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US-09-747-348-2
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10203942 Publication No. US20030096370A1 GENERAL INFORMATION:
     Query Match
                                                                                              SEQ ID NO 9
LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 192
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Patent No. US20020123067A1
GENERAL INFORMATION:
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: GB 0003502.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION FILE REFERENCE: B45210
                                                                                                                                                                                                                                                                                                                                     APPLICANT: BERTHET, FRANCOIS-XAVIER APPLICANT: DENOEL, PHILIPPE APPLICANT: POOLMAN, JAN APPLICANT: THONNARD, JOELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/171,525
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 4
                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                     PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/747,348
CURRENT FILING DATE: 2000-12-22
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TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
FILE REFERENCE: 77813-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
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                                                                               TYPE: PRT
                                                          ORGANISM: Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 DSKEEKQYKSSQVAAFRNITFATDSYTIKGEENLAILTNLVHYMKKNPKATLYIEGHTDE
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38.7%;
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US-10-156-761-14808

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US-10-156-761-10274

US-10-156-761-10912

US-10-156-761-12273
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Pred. No. 6.2e-14;
     Score 176.5;
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US-09-815-242-12181
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     DВ
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Sequence 14808, A
Sequence 6891, Ap
Sequence 10274, A
Sequence 10912, A
Sequence 12273, Ap
Sequence 5603, Ap
Sequence 12181, A
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GENERAL INFORMATION:
APPLICANT: Thierry HAUSSANT
APPLICANT: Pascale JEANNIN
APPLICANT: Yves DEINESTE
APPLICANT: FranCois LAWNY
                                                                                           Sequence 2, Application US/10169953 Publication No. US20030044915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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SEQ ID NO 10782
LENGTH: 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                            148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 PNTALNYNPWIGSINAGISYRFGQGAAPVVAAPEVVSKTFS-LNSDVTFAFGKANLKPQA 251
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                                                                                                                                                                                                                                                                                 ATADETKKQNATNVRVFGFTDNLGSYAHGLTLSKKRAEAVHDQLASALGSQDVTFEVRGY 186
                                                                                                                                                                                                                                                                                                                                                        ADGATLAPAKVLDIKSVVEDLGGEERREDTNADVTFALQAEVLFPKDSPKLNPEARSRIN 126
                                                                                                                                                                                                         SEDYPIADNTSEQGRRKNRRVEVTF 211
                                                                                                                                                                                                                                            GEERPIAFGINEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                   EQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                ATATATATTITALAVLATLTLTV-PSAVADDGDPSAPPGSVTTSPPPDVDANSPGLKL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.3%; Score 149; DB 9; 24.4%; Pred. No. 6.5e-08; tive 34; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                           -----NDETVKALASKLPSLVYFDFDSDEIKPQAAAILD 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 226;
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LENGTH: 344
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 26
SOFTWARE: F88tSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.9%; Score 136.5; DB 9 Best Local Similarity 30.2%; Pred. No. 2.6e-06; Matches 35; Conservative 20; Mismatches 50
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/998,279
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,288
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BURGESS, NICOLA A.
APPLICANT: GARCIA, MIGUES M.
APPLICANT: KIRKE, DAVID F.
APPLICANT: MEYERS, NICHOLAS L.
APPLICANT: WILLIAMS, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: FR 00 00070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jean-Yves BONNEFOY
TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT
TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ginS FILE REFERENCE: GM50081
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                     Local Similarity nes 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 LKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEK
                                                                                                                                                                  267 PTQPT-VTRVV------VDN-------VVYFRINSAKIDRNQEINVYNTAEYA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE-----
                                        154 AFGTNEEAWSQ 164
                                                                                                                      95 TINQTARVLVAGHTDER-GSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPI 153
                                                                                                                                                                                                        35 PNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER
---YEENAWNR 372
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                                                                                KTN-NAPIKVVGYADEKTGTAAYNMKLSERRAKAVAKMLEKYGVSADRITIEWKGSSEQI 364
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                         12.4%; Score 107; DB 9; 30.5%; Pred. No. 0.0041;
                                                                                                                                                                                                                                                     16; Mismatches
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                                                                                                                                                                                                                                                       49;
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                                                                                                                                                                                                                                                                                             Length 380;
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; TYPE: PRT ; ORGANISM: Lawsonia intracellularis US-10-010-160-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Porphyromonas gingivalis US-09-998-279-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-010-160-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SOFTWARE: F
; SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-998-279-24
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                                                                                                                                                                                                                                                    SOFTWARE: FOR SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10010160 Publication No. US20030103999A1
                                                                                 Matches
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/998,279
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,288
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/010,160 CURRENT FILLING DATE: 2001-11-09 PRIOR APPLICATION NUMBER: AU PRI381 PRIOR FILING DATE: 2000-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Good, Robert T,

APPLICANT: King, Kendall W.

TITLE OF INVENTION: UNVEL THERAPEUTIC COMPOSITIONS FOR

TITLE OF INVENTION: TREATING INFECTION BY LAWSONIA SPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosey, Everett L. APPLICANT: Strugnell, Richa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BURGESS, NICOLA A.
APPLICANT: GARCIA, MIGUES M.
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/249,596 PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 389
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: gins FILE REFERENCE: GM50081
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                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: DAVII10.001AUS
                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 KTN-NAPIKVVGYADEKTGTAAYNMKLSERRAKAVAKMLEKYGVSADRITIEWKGSSEQI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 PTQPT-VTRVV-----VDN--------VVYFRINSAKIDRNQEINVYNTAEYA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 ---YEENAWNR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 AFGTNEEAWSQ 164
86 ANK-LKKMLMADAIPQSATGISADDVGVLL----RVNSNSTFFPGTATLTPEGKKVMGTV 140
                                       24 ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 TINQTARVLVAGHTDER-GSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 PNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFL
                                                                                   36;
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40; Conserv
                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
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MEYERS, NICHOLAS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strugnell, Richard A.
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                   10.9%;
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                                                                                 29;
                                                                                                   Score 93.5; DB 9; Pred. No. 0.058;
                                                                                 Mismatches
                                                                                 70;
                                                                                                                      Length 237;
                                                                                 Indels
                                                                                 19;
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US-08-424-550B-605

APPLICANT: APPLICANT: APPLICANT:

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-424-550B-605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: /vo -- TELEPHONE: /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                         410 ASFIP-----
                                                                                                                                                                                                                                   360 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC 409
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                                                                                                                                                  63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                         3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60064-3500
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        RRA--VAVRNYLLG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAILDEQAQFLTTNQTARVLVAGHTD----ERGSR-EYNMSLGERRAVAVRNYLLGKGIN 138
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100 ABBOTT PARK ROAD
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SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEORGE J. DAWSON
GEORGE G. SCHLAUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOHN N. SIMONS
TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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THOMAS P. LEARY
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                                                                                                                                                                                                                                                                                                                                                                                                  48;
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RESULT 10
US-08-424-550B-394
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US-08-424-550B-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonomics
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STRANDEDNESS: si
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T: JAMES C. ERKER
T: SHERI L. BUIJK
T: ISA K. MUSHAHWAR
INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
INVENTION: REAGENTS AND METHODS FOR THEIR USE
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GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
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28.4%;
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Pred. No. 3.
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Matches Query Match Best Local :

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RESULT 11
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GENERAL INFORMATION:
APPLICANT: Hong, Zhi
APPLICANT: Butkiewicz, Nancy J.
APPLICANT: Zhong, Weidong
APPLICANT: Ingravallo, Paul
                                                                                                     Sequence 2, Application US/09742659 Patent No. US20010034019A1
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INFORMATION FOR SEQ ID NO: 394:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 55;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: SHERI L. BUJJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E |
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
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CORRESPONDENCE ADDRESS:
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GEORGE G. SCHLAUDER
SCRESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
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TAMI J. PILOT-MATIAS
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1566 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC 1615

63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122

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US-09-742-659-6
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Best Local Similarity
Whiches 38; Conserva
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US-09-742-659-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 2864
; TYPE: PRT
; ORGANISM: GB virus-B
US-09-742-659-2
                                         Matches
                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                  SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09742659 Patent No. US20010034019A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                            LENGTH: 2865
TYPE: PRT
ORGANISM: GBV-B/HCV
FEATURE:
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/742,659
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/171,469
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CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/171,469
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lemon, Stanley M.
TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
FILE REFERENCE: ID01116
                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                        NAME/KEY: SITE
LOCATION: (2275)..(2865)
OTHER INFORMATION: chimeric region
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                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
3 LHIQIAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                    PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                        Lemon, Stanley M.
VENTION: Chimeric HCV/GBV-B viruses
                                                                                                                                                                                                                                                                                                                                                                                                                             Lau, Johnson Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Butkiewicz, Nancy J.
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                                         Conservative
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                                                        10.2%; Score 87.5; Di 28.4%; Pred. No. 8.8;
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28.4%; Pred. No. 8.8;
ative 17; Mismatches
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                                    17; Mismatches
                                                                        DB 10;
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                                  Indels
                                                                        Length 2865;
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                                    Gaps
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RESULT 14
US-09-841-132-177
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US-09-886-468-21
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Sequence 177, Application US/09841132 Patent No. US20020061848A1
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SEQ ID NO 21
LENGTH: 871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/114,061
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/886,468 CURRENT FILING DATE: 1999-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-12-23
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/114,059
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                                                                                                                              532 TNLLFSGNKATGPSNSSANQEGCGGAILSFLESASVS--TKKGLWIEDNENVSLS 584
                                                                                                                                                                                                                477 ----LTFDGNTAGTSGGAIYTETEDFTLTGSTGTVTFSTNTAKTGGALYSKGNNSLSGN
                                                                                                                                                                                                                                                                                                   426 AILAFIDSGSVSDKTGLSIANNQEVSLTSNAATVSGGAIYATKCTLTGNGS-----
                                                                                                                                                                      123 RRAVAVRNYLLGKGINQASVE-----IISFGEERPIAFGTNEEAW-SQNRRAELS 171
                                                                                                                                                                                                                                                        67 PSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY---NMSL-GE 122
                                                                                                                                                                                                                                                                                                                                           15 SVLTFM-----TGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKL 66
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                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 82; DB 10; Length 871; 24.0%; Pred. No. 6.2;
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    RESULT 16
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US-09-841-132-191
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NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 177
LENGTH: 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 191
LENGTH: 977
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
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APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Chlamydia
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397 ITVASSSGEILLGAGSSQNLIFYDPIEVSNAG----VSVSFNKEA 437
                                              126 VAVRN----YLLGKGINQ-----ASVEIISFGEERPIAFGTNEEA 161
                                                                                                       348 KGGAIYIDGTSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VAVRN----YLLGKGINQ-----ASVEIISFGEERPIAFGTNEEA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 KGGAIYIDGTSN-----SKISADRHAIIFNENIVTNVTNANGTSTSANPP------RRNA 383
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                                                                                                                                                                                                               290 ASDGGAIKYTTRLDYTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 347
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                                                                                                                                                        66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
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Similarity 23.6%;
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                                                                                                     ---SKISADRHAIIFNENIVTNVTNANGTSTSANPP
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9543
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                                                                                                                                                                                                                                                                  ; ORGANISM: Streptomyces avermitilis US-10-156-761-9543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Chlamydia pneumoniae US-10-007-693-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-007-693-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9543, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.3%; Score 80; DB Best Local Similarity 24.5%; Pred. No. 2.9; Matches 37; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 157
SEQ ID NO 74
LENGTH: 361
                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 74, Application US/10007693 Patent No. US20020146776A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTIFILE REFERENCE: 210121.515C2
CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                              LENGTH: 42
TYPE: PRT
                                                                                                                                                                                                    Local Similarity
                                                                                    172 EIAAKGVGLTIDTLGLVPNSKLSKQLSCIAEA----TGGTYTSVEHKEDLTDKVNQLVDR
228 AADKVVTPVAVDGAADCAKAPTLKSGLFTDRAEFAQHRWYRVDVKPGQELRASVSLSADR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 DLGGSEKPCYVVGKNIEENSIYIVR-GEDHP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 AVRN----YLLGKGINQASVEIISFGEERP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 GNVI--DWDTKEIVGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 SALHNVLFPLGEMNKTEVRAIAAQAALPTAEKKDSTGICFIGKRPFKEFLE--KFLPNKT 215
                                           63 -ASKLPSLVYFDFDSDEIKPQA--AAILDEQAQF-----LTTNQTARVLVAGHTDE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 PSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AALSVLTFMTGCANKSTSQVMVAPNA-PTG----YTGVIYTGVAPLVDNDETVKALASKL 66
                                                                                                                             6 QIAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL---
                                                                                                                                                                                                                                                                                                                                     420
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HORIKAWA, HIROSHI
                                                                                                                                                                                Conservative
                                                                                                                                                                         9.3%; Score 80; DB
23.4%; Pred. No. 3.6;
7ative 33; Mismatches
                                                                                                                                                                                                                       DB 9;
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                                                                                                                                                                                                                    Length 420
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                                                                                                                                                                             Indels
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US-10-156-761-13758
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LENGTH: 877
                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                     Sequence 14076, Application US/09815242 Patent No. US20020061569A1
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Best Local
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APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identificat TITLE OF INVENTION: Prokaryote
                                                                                                                                                                  APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                448 EVGADRAAEVVALLSEEPPREYGDDLAAAWRAARRGGDAY 487
                                                                                                                                                                                                                                                                                                                                                                                                     134 GKGINQASVEIISFGEERPIAFGTN-EEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 RASQAAGRQRAGRAGREAPGTVYRCWAEAEDARLPRFPSPEIKVADLTAFALQAACWGDP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 APAAVQDAVLSPGAGRRVVLATSVAESSLTVPGVRVVVDCGLAREPRVDHARGLSALTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 QVSH 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 ELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 QVNPDYGVLL----RAVTVHNREIVRGEAAGTGRTDVVSTGLRYPKAESDDEDATAETVCL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 RGSREYNMSLGERRAVAVRN--YLLGKGINQASVEIISFGEERPIAFGTNEEAWSONRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 QAQFLT-----TNQTARVLV-----AGHTDERGSREYNMSLGERRAVAVRNYLL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AAAALSVLTFMTGCANKSTSQVMVAPNAPT--GYTGVIYTGVA--PLVDNDETVKALAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
53; Conserv
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                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                 Carr, Grant J.
                                                                                                         Trawick, John D.
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HORIKAWA, HIROSHI
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                        Identification of Essential Genes
Prokaryotes
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24.1%; Pred. No. 19;
Live 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
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RESULT 20
US-09-828-423-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09828423 Patent No. US20020099178A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 8.9%;
Local Similarity 22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE: ELITRA.011A
                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: WORD Perfect 6.1/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/828,423
FILING DATE: 05-Apr-2001
                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                       Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer L. Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 HLNRQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 SQNRR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 VTEDHMDR-YPFGLQQYRAAKLRVYEKAKVCVVNADDALTMPVRGADERCVSFGVNMGDY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTDERGSREYNMSLGERRAVAVRNYLLGK----GINQASVEIISFGEERPIAFGTNEEAW 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GVGGNIG----
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                                                                                                                                                                                                                             STATE: CA
  CLASSIFICATION:
                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                      INHIBITOR HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LPALMLLDADRELYVLELSSF---QLETTSSLQAAAATVLN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 76.5;
Pred. No. 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                                                                           US-10-156-761-13516
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSI
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 13516
LENGTH: 155
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2001-204089
                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0505 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
127 AVRNYLLGKGINQASVEIISFGEERPIAF-----GTNEEAWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 HFEIEVDIFEPQGISMLDAEASFITNDLLGSALTKSFSGKKGHVSFKPSLDQQRS 231
                                                       52 -----KCKPDIQTDADEIRQAVCKSTSRKFILATFATDRGQREW---LNEAKDY 97
                                                                                                67 PSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 YFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                           9 VAGAAVALLAL---TGCGGSSGSDDGAAKAVPATATG--
                                                                                                                                                                                  7 IAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKL 66
                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                               Similarity
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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25.5%; Pred. No.
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US-09-815-242-5697; Sequence 5697, Application US/09815242; Patent No. US20020061589A1
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SEQ ID NO 5697
LENGTH: 794
                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                    Sequence 12668, Application US/09815242 Patent No. US20020061569A1
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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APPLICANT: Ohlsen, Ka
APPLICANT: Zyskind,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
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                                                                                                                APPLICANT:
                                                                                                                              APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/257,931
     APPLICANT:
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nes 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                      499 TITNGRPVVTDYHGDDQTLQLLATA---
                                                                                                                                                                                                                                                                                                                                                                                                                            439 ALVASISVLVIACPCALGLATPTSIMVGTGRAAENGILFKGGEFVERTHQIDTIVLDKTG
                                                                                                                                                                                                                                                                               550 TTFKAVPGHGIEATIDHHHILVGNRKLMADNDISLPKHIS 589
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                                                                                                                                                                                                                                                                                                               99 TARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGIN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AAAAALSVLTEMTGCA--NKSTSQVMVAPN--APTGY----
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Zyskind, Judith W.
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Yamamoto, Robert T
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                   Carr, Grant J.
Yamamoto, Robert T
                                                     Trawick, John D.
                                                                        Wall, Daniel
                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
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     H. Howard
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23.8%; Pred. No. 27;
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LENGTH: 1330
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Query Match
Best Local Similarity
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TYPE: PRT
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; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-10510
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                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SAKAKI, YOSHIYUNI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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Local Similarity 23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 ALVASISVLVIACPCALGLATPTSIMVGTGRAAENGILFKGGEFVERTHQIDTIVLDKTG 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Pred. No. 27;
Score 74.5;
Pred. No. 72;
                       DB
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                       9;
                       Length 1330;
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RESULT 26
US-10-128-714-8493
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US-10-128-714-3493
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                                                  Sequence 8493, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PELICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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Best Local (
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SEQ ID NO 3493
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APPLICANT:
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         APPLICANT: Jiang, Bo APPLICANT: Hu, Wenqi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and TITLE OF INVENTION: Methods of Use FILE REFERENCE: 10182-018-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690 PLLLDQTAGWL-----
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                                                                                                                                                                                                                                                                                                                                                                                                          72 FDFDSDEIKPQAAAILDEQAQFLTTNQ-----TARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                               42 LDAICFVLGITNMSTVRAQNLQDLIYKRGQAGVTKASVTIVFDNRDTAKSPIG-----
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Tishkoff, Daniel
Zamudio, Carlos
Eroshkin, Alexey M
Lemleux, Sebastien M
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                                                                                                                                                                                                       NNPNFLIMQGRITKVLNMKPVEILSMIEE---AAGT 171
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23.1%; Pred. No.
                                                                                                                                                                                                                                                                                          ---FEEYATISVTRQIVLGGTSKYLINGHRAQQQTVQ-NLFQSVQLNI 138
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Mismatches
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6179
LENGTH: 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6179, Application US/09738626
Publication No. US20020197605A1
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Best Local :
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APPLICANT:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Excentian, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
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CURRENT FILING DATE: 2002-04-23
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Local Similarity 23.1%; Pred. No.
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                                                                                                                                                                                                                                                                                                            IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                      SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                          YOKOI, HARUHIKO
TATEISHI, NAOKO
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US-09-815-242-10417
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                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10417
LENGTH: 928
TYPE: PRT
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                                                                                                                                                                                                     Query Match
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APPLICANT:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                  Local Similarity
  369 VGLSFAIEPGVAAYIPVAHDYLDAPDQISR-----
                                                                          310 ETSVADEAPEVTATVISYDNYVTILD-EETLKAWIAKLEKAPVFAFDTETDSLDNISANL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 GDQDRRLTISEQ----ITNYDHGEVVDEDTVR-FHFSEPAP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 GSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERP 152
                                                                                                                30 QVMVAPNAPTGYTGVI-YTGVAPLVDNDETVKALASKLPSLVYFDFDSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 SLVYFDFDSDEIKPQAAAIL---DEQAQFLTTNQTARVLVAGHTD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AAAATLAGLAVLSGCTAQPSQAEDNTLTYLEPQFFRTLYPPSAGFYPNGSVVNNIADR-- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AAAAALSVLTEMTGC-ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLP 67
                                     -----EIKPQAAAILDEQAQFL-TTNQTARVLVAGHTDERGSREYNMSLGERRAVAV-RN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LLYQDPETLELKPWIATELPEVNEDATEFTFNIRTDVTYSDGTPLTAENVVKNFDLYGL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall, Daniel
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5%; 5c.
23.6%; Pred
3.6%; 27;
                                                                                                                                                                              8.5%; Score 73.5; DB 10; 26.3%; Pred. No. 55;
                                                                                                                                                             23;
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Pred. No. 27;
                                                                                                                                                             Mismatches
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                                                                                                                                                         57;
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--ERALELLKPLLEDEKALKVGQN 420
                                                                                                                                                           Indels
                                                                                                                                                                                                 Length 928;
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RESULT 29
US-10-071-179-29
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; LENGTH: 1312
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/071,179
CURRENT FILING DATE: 2002-02-07
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              LOCATION: 808..811
OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                           LOCATION: 1226..1228
OTHER INFORMATION: potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 755..757 OTHER INFORMATION:
FEATURE:
                                                          NAME/KEY: PHOSPHORYLATION
                                                                                       FEATURE:
                                                                                                        OTHER INFORMATION: potential
                                                                                                                                   NAME/KEY: PHOSPHORYLATION LOCATION: 663..666
                                                                                                                                                                                                   OTHER INFORMATION: potential
                                                                                                                                                                                                                                               NAME/KEY: PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: potential
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LOCATION: 1151..1153
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OTHER INFORMATION: potential
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LOCATION: 294..296
OTHER INFORMATION: potential
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                                                                                                                                                                               FEATURE:
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NAME/KEY:
LOCATION:
                                                                                                               NAME/KEY: PHOSPHORYLATION LOCATION: 888..890 OTHER INFORMATION: potential
                                                                                                                                                                                            NAME/KEY: PHOSPHORYLATION LOCATION: 876..878 OTHER INFORMATION: potential
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                                                                                                                                                                                                                                                                    NAME/KEY: PHOSPHORYLATION LOCATION: 815..817 OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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                      FEATURE
                                    OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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NAME/KEY: PHOSPHORYLATION
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OTHER INFORMATION: potential
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THER INFORMATION: potential
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THER INFORMATION: potential
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NAME/KEY: PHOSPHORYLATION
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OCATION: 41..43
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AME/KEY: PHOSPHORYLATION
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                                                          PHOSPHORYLATION 939..941
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                                          Matches
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Best Local S
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LOCATION:
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OTHER INFORMATION: potential
                                                                                                                  NAME/KEY: PHOSPHORYLATION LOCATION: 295..298
                                                                                                                                                                       NAME/KEY: PHOSPHORYLATION
LOCATION: 276..279
OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                       FEATURE: PHOSPHORYLATION LOCATION: 274..277
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PHOSPHORYLATION LOCATION: 159..162
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential FEATURE:
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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    27 STSQVMVAPNAPTGYTGVIYTGVA------PLVDNDETVKALASKLPSLVYFDFDS
                                                            Similarity
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1208..1210
                                        Conservative
                                        8.5%; Score 73; DB 22.1%; Pred. No. 1e+(tive 22; Mismatches
                                                            DB 9;
le+02;
                                              60;
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20 Вb

1076 GELQDLQSEGNSSPAGFDASYSSSSSNQPEPEHPEKACTGQKRVKDAQGGGSSSKKQKRS 1135

Length 1312; Indels

38;

Gaps

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US-09-815-242-12162

Sequence 12162, Application US/09815242

Patent No. US20020061569a1

; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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Best Local
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              APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 32; Conserv
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                                                                                                                                                                                                                                                                 495 SLFNY 499
                                                                                                                                                                                                                                                                                                             127 AVRNY 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                    375 VVDVPESNVAFKGQLNPGKLLLVDFKQNKVIENNDLKGAIAGELPYKAWIDNHKVDFDFE 434
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Yamamoto, Robert T.
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Zyskind, Judith W.
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25.6%;
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Pred. No. 1.2e+02;
"" wismatches 50;
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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SEQ ID NO 12162
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                                      CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                               APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-02 10
NUMBER OF SEQ ID NOS: 14110
NUMBER OF SEQ FOR Windows Version 4.0
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NUMBER OF SEQ ID NOS: 7059
                       PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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TATEISHI, NAOKO
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Yamamoto, Robert T.
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25.6%; Pred. No.
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Version #1.25

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; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4444
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                  ; Sequence 2, Application US/09901106
; Patent No. US20020151067A1
                                                            RESULT 34
US-09-901-106-2
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US-10-156-761-9933
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LENGTH: 851
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA,
APPLICANT: IKED!
APPLICANT: ISHII
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                86 ILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEII 145
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HORIKAWA, HIROSHI
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SAKAKI, YOSHIYUKI
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21.1%; Pred. No. 62;
vative 19; Mismatches
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Pred. No. 1.3e+02;
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US-10-156-761-13680
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
APPLICANT: SHIBA, TADAYOS
APPLICANT: SAKAKI, YOSHIY
APPLICANT: SAKAKI, YOSHIY
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 13680, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                     APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-252
                                      CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
  PRIOR FILING DATE: 2001-09 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 828-103P TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/920,281C FILING DATE: 11-AUG-1992 ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/901,106
FILING DATE: 10-Jul-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA Expression Systems Based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Garoff, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1799 SGITFGDFDDVLRLGRAGAYIFSSDTG----SGHLQQKSVRQHNLQCAQLDAV 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1756 ASRAAERPVPAPRKPT------PAPRT-----AFRNKLP-LTFGDFDEHEVDALA 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 AAI------LDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                 ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                        2001-05-30
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23.0%;
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  JP 2001-272697
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Pred. No. 2.8e+02;
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Mismatches

DB 10; 36;

Length 2431; Indels

31;

Gaps

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; SEQ ID NO 13680
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13680
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                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptomyces avermitilis US-10-156-761-14476
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US-10-156-761-14476
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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Best Local Similarity
Matches 46; Conserv
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LENGTH: 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14476, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                              Query Match
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APPLICANT:
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                            Local
                             137 INQASVEIISFGEERP 152
                                                                                                                                         245 FTGGLHTGRRLMAAAAGTYKKVALELGGKNPNIVFADADFDTAVDMALTAVFLHSGQVCS
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362 LDEGAV--LRCGGRRP 375
                                                                  305 AGARLLVEDSLHDRFVDEVVRRAAEIRLGGPFDERAQTGALISAAHRAKVEA---YVAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 FIGPWAPVSLG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 ADSTADPVHVASDLISQAEHDPLAAAVLVTDSVELADAVEKELEPQVAATKHIDDRIVPA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 EVYAAGGATAVAMFAYGTESCAPADMVTGPGNIWVAAAKRYFTGKIGIDAEAGPTEIAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 LTTNQTARVLVAG------HTDERGSREYNMSLGERRAVA--VRNYLLGKGINQASVEII 145
                                                                                                                                                                           41 YTGVIYTGVAPLVDNDETVKALASKL----PSLYYFDFDSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 QAAAILDEQA----QFL--TTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKG 136
                                                                                                                                                                                                                        l Similarity
32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKGRQSATVLVDGVDEGLRVVDAYGAEHLEIQTADAAAVADRVRN----
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                        8.3%; Score 71.5;
23.5%; Pred. No. 3
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24.1%; Pred. No. 31;
Live 21; Mismatches
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                          DB 9;
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                                                                                                                                                                                                                                                          Length 507;
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                                        ; ORGANISM: Homo sapiens US-09-925-301-908
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                                                                                                  ; SOFTWARE: Pate
; SEQ ID NO 908
; LENGTH: 248
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LENGTH: 2862
TYPE: PRT
ORGANISM: GBV-B/HCV
                                                                                                                                                                                                                                                                                                                                                                                Sequence 908, Application US/09925301 Patent No. US20020052308A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
Query Match
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION 1999-03-12
                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/742,659
CURRENT FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT:
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                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lemon, Stanley M.
TITLE OF INVENTION: Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: SITE
LOCATION: (945)..(1129)
OTHER INFORMATION: chimeric region
                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (1579)..(1593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: chimeric region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 8.3%; Score 71.5; DB 10; Local Similarity 27.5%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1651 FLGPHAATILAIIEYCCG 1668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 SLGERRA--VAVRNYLLG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVA----PNAPTGYTGVIYTGVAPLVDNDET 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                 PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhong, Weidong
Ingravallo, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Butkiewicz, Nancy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hong, Zhi
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8.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
Score 71;
DB 10;
Length 248;
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RESULT 40
US-09-997-181-133
; Sequence 133, Application US/09997181
; Publication No. US20030049269A1
; GENERAL IMPORMATION:
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CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR PILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 09/000,254
PRIOR APPLICATION NUMBER: 09/000,254
PRIOR APPLICATION NUMBER: 09/000,254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 133, Application US/09996634 Patent No. US20020172684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
                                                           CURRENT APPLICATION NUMBER: US/09/997,181
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
                                                                                                                                                                               TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61257
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
                                                                                                                                                                                                                                                    APPLICANT: Nano, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 FGEAK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 FGEER 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 -----KLPSLVYFDFDSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 ETVPATEQELPQPQAETGSGTESDSDESVPE----LEEQDSTQATTQQAQLAAAAEIDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                 75 VVVTVNNLSTLPFESVDADVTNQPQGNGQAVGNAKVRMKPNTPVVATE---FLVTNKT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 PVSKAKQSRSEKKARKAMSKLGLRQVTGVTRVTIRKSKNILFVITKPDVYKSPASDTYIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 ETVKALASKLPSLVY-----FDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 IAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALAS-- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAILIAATLFATVVAGCGKKPTTASSPSPGSPSPEAQQI-----LQDSSKATKGLHSVH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 259;
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Search completed: July Job time : 308 secs
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                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 133
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                          LENGTH: 25
                                                                                                                                                                                                                                   Match 8.2%;
Local Similarity 23.7%;
                                                                                                           65 -----KLPSLVYFDFDSD-----
                                                                                                                                             21 VAILIAATLFATVVAGCGKKPTTASSPSPGSPSPEAQQI-----LQDSSKATKGLHSVH 74
                                                                       75 VVVTVNNLSTLPFESVDADVTNQPQGNGQAVGNAKVRMKPNTPVVATE---FLVTNKT 129
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                                                                                                                                                                                                                    Conservative
               6, 2003, 14:19:27
                                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                    Score 71;
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16;
                                                                                                         ---EIKPQAAAILDEQAQFLTTNQT 99
                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                    Indels
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-O-/cgn2_f/USPTO_spool/VGS06/74779/runat_06072003_121614_9825/app_query.fasta_1.327
-DB-Issued_Patents_NA -OFMT-fastap -SUFFIX=p2n.rn1 -MINVATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi
-LIST=100 -DCCALIGN=200 -THR_SCORE=PCt -THR_MAX=100 -THR_MIN-0 -ALIGN=40
-LIST=100 -DCCALIGN=200 -THR_SCORE=PCt -THR_MAX=100 -THR_MIN-0 -ALIGN=40
-MODE-LOCAL -OUTPMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                  Result
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Maximum Match 100%
Listing first 100 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primand is derived by analysis of the total score distribution.
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1: /cgn2_5/ptodata/1

2: /cgn2_5/ptodata/1

3: /cgn2_5/ptodata/1

4: /cgn2_5/ptodata/1

5: /cgn2_5/ptodata/1

6: /cgn2_6/ptodata/1
                                                                                                                                                                                                                                                                                     Query
Match
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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861
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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                                                                                                                                                                                                                                                                                         Length DB
                                                                      867
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                      US-07-807-049-1
US-08-476-102A-3
US-08-572-447C-12
US-09-267-747-12
US-09-267-747-10
US-08-572-447C-14
US-08-572-447C-14
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1 US-08-455-246-14
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US-09-221-017B-786
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Sequence 786, App
Sequence 776, App
Sequence 2, Appli
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RESULT 1
US-08-743-637B-178
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Score:
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                                                       US-08-743-637B-178
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                                                                                                                                                               APPLICATION NUMBER: US 08/526,840
APPLICATION NUMBER: US 08/526,840
FILLING DATE: 11-SEP-1995
AFTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 360586.900.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEPHONE: (414) 277-5901
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                               TOPOLOGY:
                                                                                                                             STRANDEDNESS:
                                                                       ORGANISM:
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SYSTEM: PC-DOS/MS-DOS
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                                                                    Haemophilus influenzae
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US-08-854-585-1
PCT-US95-05512-1
US-08-809-267-9
PCT-US95-13662A-9
US-08-110-786A-7
US-08-110-786A-7
US-08-288-381A-6
US-09-453-7028-27
US-08-784-582-57
US-08-784-582-70
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    Length: Matches:
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TITLE OF INVENTION: DNA PROBE FOR THE IDENTIFICAT
OF HAEMPHILUS INFLUENZAE
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 932,872
                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 08-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-NOV-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 GAACGTGGTACACCAGAATACAACATCGCATTAGGACAACGTCGTGCAGATGCAGTTAAA
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                                                                                                                                                                                 151 GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTTCAAATCTTAGATGCG
          331 GGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA 390
                            130 AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                          211 CACGCAGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTAGAAGGTAATACTGAT
                                                                                                                                                                                                         70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                                    90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
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                                                                                GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
                                                                   GAACGTGGTACACCAGAATACAACATCGCATTAGGACAACGTCGTGCAGATGCAGTTAAA
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US-07-807-049-1
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NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/92,948

FILING DATE: 08-0CT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Patent No. 5173294
; APPLICANT: MURPHY,TIMOTHY F.;APICELLA, MICHAEL A.
; TITLE OF INVENTION: DNA PROBE FOR THE IDENTIFICATION
                                                                                                                                                                                         Sequence 1, Application US/07807049 Patent No. 5300632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:1:
                                                                                                                                                                       GENERAL INFORMATION:
                                                                 APPLICANT: Murphy, Timothy F
APPLICANT: Apicella, Michael A
TITLE OF INVENTION: A Method for Purifying an Outer Membrane
TITLE OF INVENTION: Protein of Haemophilus Influenzae
NUMBER OF SEQUENCES: 1
                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
ADDRESSEE: Alan ... Tower STREET: 1600 Empire Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 867
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                                   Alan S. Korman, Esq
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264.00
68.93%
49.51%
30.66%
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (716) 853-810
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 08-OCT-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                      DOCUMENT NUMBER: US 4,474,758
FILING DATE: 02-OCT-1984
PUBLICATION IMPORMATION:
                                                                                                                                                     PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 4,427,782
FILING DATE: 24-JAN-1984
       PUBLICATION INFORMATION:
                                                                                                                                PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 853-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAP POSITION: Unknown PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18 NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: KORMAN ESQ., ALAN S
REGISTRATION NUMBER: 32,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: |
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
AUTHORS:
AUTHORS:
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DATE:
                     PUBLICATION DATE: 01-OCT-1986
RELEVANT RESIDUES IN SEQ ID NO:
                                                         DOCUMENT NUMBER:
                                                                                                                                                                                                                                                VOLUME:
                                                                                                                                                                                                                                                                  JOURNAL:
                                                                                                                                                                                                                                                                                       TITLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY:
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HAPLOTYPE: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Buffalo
STATE: NY
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Molecular Analysis of P6: The cloning and sequencing of an Outer Membrane Protein Haemophilus Influenzae
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US-08-476-102A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent
TELEX: 301-309-8 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
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PUBLICATION DATE: 01-SEP-1985
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fleischmann, et al. TITLE OF INVENTION: Nucleotide Sequence of the Haemphilus
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                          NAME: MAYKS, Michelle S.
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTTCAAATCTTAGATGCG 429
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Ave.
                                                                                                                                                               FILING DATE: 07-Jun-1995 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                            STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
                 TELEPHONE: 301-309-8504
TELEX: 301-309-8439
                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                        APPLICATION NUMBER: US/08/476,102A
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08572447C Patent No. 5955090
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                 APPLICANT: Domdey, Horst TITLE OF INVENTION: ImmuriTITLE OF INVENTION: Deri
            COMPUTER READABLE FORM:
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                  ZIP:
                                                 COUNTRY:
                                                                                            CITY: Washington
                                                                                                                  STREET:
                                                                                                                                   ADDRESSEE:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
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LENGTH: 1059 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             577 CCAAATACCGCACTTAACTACAACCCTTGGATTGGTTCTATCAATGCGGGTATTTCTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814 GTTGCTGGTTACACTGACCGTATTGGTTCTGACGCGTTCAACGTAAAACTTTCTCAAGAA 873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 AlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 SerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAla
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                                  20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
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                                                                       D.C
                                                                                                                  1300 I Street, N.W.,
                                                                                                                                                                                                                                                                                Von Specht, Bernd-Ulrich
                                                        USA
                                                                                                                                                                                                                                                                                                                       Hungerer, Klaus-Dieter
                                                                                                                                                                                                                                                                                                                                          Knapp, Bernhard
                                                                                                                                                                                                                                                                                                     Broker, Michael
                                                                                                                                                         Finnegan, Henderson, Farabow,
                                                                                                                                        Dunner
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30.57%
20.50%
                                                                                                                                                                                                                   Immunogenic Hybrid Protein OprF-OprI
Derived From Pseudomonas aeruginosa Membrane Proteins.
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MEDIUM TYPE:

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US-09-674-779B-2 (1-172) x US-08-572-447C-12 (1-645)
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Patent No. 5955090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
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NAME: M. Paul Barker REGISTRATION NUMBER: 32,013 REGISTRATION NUMBER: 32,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: C-terminus and oprI without signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
TISSUE TYPE: Serotype 6; ATCC 33354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                           325 GTTCGTGACGTACTGGTCAACGAGTACGGTGGGAAGGTGGTCGCGTGAACGCTGTCGGT 384
                                                                                                                                                                      108 ThraspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla 127
                                                                                  128 ValArgAsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                               265 ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC 324
                                                                                                                                                                                                                   205 AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                                                                                                                     145 CTGGACGTGAAGTTCGACTTCGACAAGTCCAAAGGTCAAAGAGAACAGCTACGCTGACATC 204
                                                                                                                                                                                                                                                                                                                                                                                          85 GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                     57 GluThrValLysAlaLeuAlaSerLysLeuProSerLeu--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
                                                                                                                                                                                                                                                          AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
                                                                                                                                                                                                                                                                                                                                                 -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu 87
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Alignment Scores: Pred. No.:
                                                                                   OTHER INFORMATION: C-terminus and oprI without signal sequence " US-09-267-747-12
 Percent Similarity:
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                                                                                                                  Patent No. 6300102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/572,
FILING DATE: 14-DEC-1995
APPLICATION NUMBER: EP 941200:
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: M. Paul Barker
REGISTRATION NUMBER: 32,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                 HYPOTHETICAL: NO ANTI-SENSE: YES
                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                              OTHER INFORMATION:
                                                                                                                                                   LOCATION:
                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                  TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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E: Serotype 6; ATCC 33354
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Broker, Michael
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16-DEC-1994
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175.50
46.58%
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                                                                                                                         /note= "Sequence is coding for oprF
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Query Match:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                       APPLICATION NUMBER: FILING DATE: 14-DE
                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             STREET: 1300 I S:
CITY: Washington
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                     CLASSIFICATION: 424
                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT 264
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5955090
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Broker, Michael
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Best Local Similarity:
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                                                                         US-09-267-747-10
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                 Sequence 10, Application US/09267747
Patent No. 6300102
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
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 APPLICANT:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                   ValArgAsnTyrLeuLeuGlyLys----GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                                                                                                                                                                                                                                                        ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                                                                                                                                                                                                                                                                             ThraspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla 127
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCGCTTGAAGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu 87
                                                                                                                                  CGCGTTGAA
                                                                                                                                                                       ArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
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E: Serotype 6; ATCC 33
Knapp,
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                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: US-09-267-747-10
                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Patent No. 6300102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: M. Paul Barker
REGISTRATION NUMBER: 32,013
REGISTRATION NUMBER: 32,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: (HYPOTHETICAL: NO ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Domdey, Horst
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 14-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
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91 GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG 150
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E: Serotype 6; ATCC 33354
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Broker, Michael
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US-08-572-447C-14
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                                                                                                                               TELEFAX: (202) 408-440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 14-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
MOLECULE TYPE: HYPOTHETICAL:
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                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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ADDRESSEE: Dunner
                                                                                                               LENGTH:
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                                                                                                          681 base pairs
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                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-267-747-14
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OTHER INFORMATION:
                                                                                                                                                                                                                                                          Patent No. GENERAL I
                                                                                                                                                                                                                                                                                              Sequence 14,
                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                         APPLICANT: Broker, Michael
APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Lomdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa I
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE: FEATURE:
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 STREET:
CITY: W
STATE:
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LOCATION: 1..678
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                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
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                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                           4, Application US/09267747 6300102
Washington D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                         ArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGGCGAGTCCCGCCCGGTTGCCGACAACGCCACCGCTGAAGGCCGCGCTATCAACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTTGGTCGCGTGAACGCTGTCGGT
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                                     1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                      Hungerer, Klaus-Dieter
                                                                                                                                                                                                                                         Knapp, Bernhard
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E: Serotype 6; ATCC 33354
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171.50
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; OTHER INFORMATION:
US-09-267-747-14
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Best Local Similarity:
                    В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: HYPOTHETICAL: NO ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-DEC-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/O FILING DATE: 14-DEC-1995 APPLICATION NUMBER: EP 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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                                                                                                                                                                   CTGGACGTGAAGTTCGACTTCGACAAGTCCAAGGTCAAAGAGAACAGCTACGCTGACATC
                                                                                                                                                                                                                                           GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG
                                                                                                                                                                                                                                                                           GluThrValLysAlaLeuAlaSerLysLeuProSerLeu---
                      ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                 AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
                                                                                             AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                   -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
1.678
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E: Serotype 6; ATCC 33354
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16-DEC-1994
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46.15%
33.57%
19.92%
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US-09-674-779B-2 (1-172) x US-08-457-997B-1 (1-1720)
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Best Local Similarity:
                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                               US-08-457-997B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08457997B Patent No. 5766608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 522-8458
                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kolattukudy, P. E. TITLE OF INVENTION: Otitis Media Vaccine
                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: no
STRAIN: 1128
                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                     1001 CCAAATACCGCAATTAACTACAACCCTTGGATTGGTTGTATCAATGCGGGTATTTCTTAC 1060
                                                              35 ProAsnAlaProThrGlyTyr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526 GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTGGTCGCGTGAACGCTGTCGGT 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1720 base pairs
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Suite 1800 800 Superior Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
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29.94%
19.22%
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                                                                                                                                       Gaps:
                                                                                                                                                                        Mismatches:
                                                                                                                                                           Indels:
                                                                                                                                                                                              Conservative:
                                                            ----ThrGlyValIleTyr 46
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US-08-467-722A-1
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                                                                                                                                                                                                                                      TELEFAX: (216) 241-08
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLTICK, MATY E.
                                      FEATURE:
                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                          ANTI-SENSE:
                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
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 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Survey CITY: Cleveland
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                                                      STRAIN:
                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                 TOPOLOGY:
                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 IleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 SerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAla 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                              nucleic acid
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                                                        1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Calfee, Halter and Griswold
Suite 1800 800 Superior Avenue
CDS
407..1483
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VENTION: Otitis Media Vaccine
                                                                 non-typable Haemophilus influenzae
                                                                                                              ŏ
                                                                                                                                           circular
                                                                                                                                                                                                                                                                           (216) 622-8458
                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                               double
                                                                                                                                                                                                                                                      241-0816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AlaTrpSerGlnAsnArgArgAlaGluLeuSer 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 786, Application US/09221017B Patent No. 6444799
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO.:
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP15
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                              CURRENT APPLICATION DATA:
                                                                              APPLICATION NUMBER: FILING DATE: 23-DE CLASSIFICATION:
                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1121 AGC---TTAAATTCTGATGTAACTTTCGCATTTGGTAAAGCAAACTTAAAACCTCAAGCA 1177
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                                                                                                                                             SYSTEM: Windows FastSEQ for Windows Version 2.0b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
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TELEX: 706141
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STRANDEDNESS: double
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US-09-674-779B-2 (1-172) x US-09-221-017B-786 (1-3656)
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                                                                                                                     2090 GCGCTGACGAAGTTTGCTGCAAACATGAACAAAAACCCCCGACACGGATATTCGTATCGTA 2031
106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
                                                                                                                                                                           86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DUA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                1003411 GGACCCCCGGCCTCCGGCCCATGTGCCGACCTGCAATCAGCCATCAATGCCGTGACGGGT 1003470
                                                                                                 1003291 ACCTTGACCGGAACTGCCCCTTCATCCGAGCACAAGGACGCAGTGAAGCGCGCGGCGACCC 1003350
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70 -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu 87
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US-09-674-779B-2 (1-172) x US-09-103-840A-1 (1-4411529)
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                              1003290 ACCTTGACCGGAACTGCCCCTTCATCCGAGCACAAGGACGCAGTGAAGCGGCGGCGGCGACC 1003349
                                                                                                                                                            1003230 GTTTTCACCGCCAGCGTGCCGATTCCTGATTTTGGCCTCAAAGTCGAAAGGGACACCGTC 1003289
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                                                                                                  45 IleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys---AlaLeuAla 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 GlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArg 167
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64 SerLysLeuProSerLeu----
                                                                                                                                                                                                                                   40 GlyTyrThrGly-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                               APPLICATION DATA: 09-APR-1000
PRIOR APPLICATION NUMBER: PCT/AU98/01023
APPLICATION 10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09
FILING DATE: 23-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 1
FILING DATE: 31-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                             FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                              APPLICATION NUMBER: PP2911 FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
US-08-743-637B-11
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                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08743637B
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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ZIP: 53202-4-2.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOPEY
MS-
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                                                                                                                                                                                           NUMBER OF SEQUENCES:
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STRANDEDNESS: double
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                                                                                  COUNTRY:
                                                                                                      STATE:
                                                                                                                                    STREET:
                                                                                                                                                        ADDRESSEE:
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OUELLETTE, Marc
ROY. Danni "
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32.538
16.498
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                                                                                                                                                                                         SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ... 273
 PC-DOS/MS-DOS
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Indels:
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Matches:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 04-NO

CLASSIFICATION:

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US-09-674-779B-2 (1-172) x US-08-743-637B-11 (1-730)
                                                                                                                                                                                               Sequence 11, Application US/08526840B Patent No. 6001564
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INFORMATION FOR SEQ ID NO: 11:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
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REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                         668 CGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATC 715
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                                                                                                                                                                                                                                                                                                                                                                 608 GCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCT 667
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                                                                                                                                    BERGERON, Michel G.
OUELLETTE, Marc
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                     SPECIFIC AND UNIVERSAL PROBES AND
AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 8509
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: QUARLES & BRADY
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Query Match:

Best Local Similarity: Percent Similarity: Alignment Scores: US-08-743-637B-11

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ORIGINAL SOURCE: MOLECULE TYPE:

STRANDEDNESS:

TOPOLOGY:

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SEQUENCE CHARACTERISTICS:

LENGTH:

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US-08-526-840B-11 RESULT 19

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:

NUMBER OF SEQUENCES:

APPLICANT: APPLICANT:

ROY, Paul H.

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INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Nguyen Ngoc, Thien
TITLE OF INVENTION: Carrier Prot
TITLE OF INVENTION: Effect, Immu
TITLE OF INVENTION: Their Prepan
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 1007 base pairs
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/836,500A
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796 CGTGCTCAGTCCGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCC 855
                                   124 ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                        736 GTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAA 795
                                                                                                             104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
                                                                                                                                                                                    86 IleLeuAspGluGlnAlaGlnPheLeuThrThr-----AsnGlnThrAlaArgValLeu 103
                                                                                                                                                                                                                                               66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
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Effect, Immunogenic Complex Containing It, Process I
Their Preparation, Nucleotide Sequence and Vaccines
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US-09-674-779B-2 (1-172) x US-08-721-979A-13 (1-1008)
                                                                                                                                                                     US-08-721-979A-13
                                                                                                                                   Alignment Scores:
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                                                  Query Match:
                                                                    Best Local Similarity:
                                                                                  Percent Similarity:
                                                                                                                     Pred. No.:
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                                                                                                                                                                                                                                                                                                                                      TELEFAX: 616-382-2030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Trudel, Michel TITLE OF INVENTION: PEPTII TITLE OF INVENTION: SYNCY: TITLE OF INVENTION: COMPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FR 9-
FILING DATE: 06-APR-1994
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
STREET: Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1..1008
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 16. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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06-APR-1994
                                                                                                                                                                                                                                                         peptide
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SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS
75
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                                                                                                                        TELEFAX: 616-382-2030 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                          NAME: Hueschen, Gordon W.
REGISTATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
               MOLECULE TYPE:
                                                                                                       SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
FEATURE:
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STREET: Avenue
CITY: Kalamazoo
STATE: MI
                               LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Raloccompations
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COMPUTER: IB
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715 The "H" Bldg., 31
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Trudel, Michel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
             peptide
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SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS
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US-08-129-719-14
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; LOCATION: 1..1008
; OTHER INFORMATION:
US-09-654-289-13
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Best Local Similarity:
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                                  TELEFAX: (716) 849-0349 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                      REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
                                                                                                                                                                                                                                             SOFTWARE: Wordperfect for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
                                                                                                                                                                                    FILING DATE: September 2 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                            NAME: Nelson, M. Buc
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                             COMPUTER: IBM Com
OPERATING SYSTEM:
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                    LENGTH:
                                                                                                                                                                                                                           APPLICATION NUMBER:
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nucleic acid
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                                                                                                                                                                                                                                                                                             IBM Compatible
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                                                                                                                                                                                                       September 29,
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NAME/REY: signal sequence of encoded protein;
LOCATION: -26 to -1
US-08-129-719-14
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                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08306871 Patent No. 5712118
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: genom
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                                                                                                                                                                                                                                                          APPLICANT: Timothy F. Murphy TITLE OF INVENTION: Vaccine For Branhamella catarrhalis NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Branhamella catarrhalis STRAIN: 25240
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COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
URRENT APPLICATION DATA:
                                                                                                                                                            STATE:
                                                                                                                                                                                                STREET:
                                                                                                                                       COUNTRY:
                                                                                                                                                                               CITY: Buffalo
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EMBL3 clone 5
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US-08-569-959-14
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             Sequence 14, Application US/08569959
Patent No. 5725862
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
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LENGTH: 1727 nucleotides
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APPLICANT:
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REGISTRATION NUMBER:
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                                                                                                                               1363 AAAGCGATGAACCGTCGTGTAGAA 1386
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Timothy F. Murphy
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Conservative:
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US-09-674-779B-2 (1-172) x US-08-569-959-14 (1-1727)
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
LOCATION: CD gene region
IDENTIFICATION METHOD: b.
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LENGTH: 1727 nucleotides
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IMMEDIATE SOURCE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1 SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
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                                                                                                                        1135 GTTGCTGCGCAAATGCGTGAATTC-----CCAAATGCAACTGCA-----ACCATTGAA 1182
                                                                                                                                                                                           1075 GTATTCTTTGATTATGATAAATCAATCATCAAACCACAATACCGTGAAGAAGTTGCTAAG 1134
123 ArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSer 141
                                                                                   106 GlyHisThrAspGlu------ArgGlySerArgGluTyrAsnMetSerLeuGlyGlu 122
                                                                                                                                                        86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                                  70 ValTyrPheAspPheAspSerAspGluIleLysProGln-----AlaAlaAla 85
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       US-09-674-779B-2 (1-172) x US-08-469-260A-80 (1-4268)
                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                          US-08-469-260A-80
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
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TELEPHONE: 708-938-2623
TELEPHONE: TONO:
                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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SHERI L. BUIJK
ISA K. MUSHAHWAR
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THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                           linear
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GEORGE G. SCHLAU
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TAMI J. PILOT-MATIAS
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US-08-469-260A-1
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TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO:
                                REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 55;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA:
                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
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GEORGE G. SCHLAUI
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Best Local Similarity:
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LENGTH: 8912 base pairs
TYPE: nucleic acid
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                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                  CITY: Abbott Park
                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                      ADDRESSEE:
CLASSIFICATION: 435
                     FILING DATE:
                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5061 ------GTCGCCCCAGTGGTTGACGAAGAGGAAATCGTGGAGGAGTGT 5102
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5955318
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                                                                                                                                                                                                                                                                                                                                                                                           Mushahwar, I. K.
                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                           Abbott Laboratories
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ATTORNEY/AGENT INFORMATION:

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TELEFA: 708-yoo ....
32:
SEQUENCE CHARACTERISTICS:
LENGTH: 9143 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                Sequence 390, Application US/08469260A Patent No. 6451578
                                                                                                                                                                                                                                               GENERAL INFORMATION:
       APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
                                                                                                                                         APPLICANT: APPLICANT:
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
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                                                                                                                   GEORGE J. DAWSON
GEORGE G. SCHLAUDER
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                           JOHN N. SIMONS
TAMI J. PILOT-MATIAS
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Gaps:
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MEDIUM TYPE: Floppy disk
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/469,260A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD
                        5414 CATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGC 5455
                                                                                        5357 ---ACTAGTCCTTTCACATTGGAAACCGCCCTTGAAAAACTTAACACCTTTCTTGGGCCT 5413
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                                                         123 ArgArgAla-----ValAlaValArgAsnTyrLeuLeuGly 134
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US-08-469-260A-393
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US-08-469-260A-393
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                                   US-09-674-779B-2 (1-172) x US-08-469-260A-393 (1-9143)
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INFORMATION FOR SEQ ID NO: 393:
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REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 9143 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ABBOTT PARK
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                                                                                                                                                                                                                                                                                                                                                LENGTH: 9143 base pairs TYPE: nucleic acid STRANDEDNESS: double
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          3 LeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly
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JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
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THOMAS P. LEARY
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US-09-556-877-171
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Best Local Similarity:
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SOFTWARE: FastSEQ for
SEQ ID NO 171
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Skeiky, Yasir
Fling, Steve
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TITLE OF INVENTION: COMPOSTIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
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CURRENT FILING DATE: 2000-04-19
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                                                                                                                                                                                                                                                                        829 GCTTCTGATGGAGGAGCAATTAAAGTAACTACTCGCCTAGATGTTACAGGCAATCGT---
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                                                                                                                                                              886 ---GGTAGGATCTTTTTAGTGACAATATCACAAAAAATTATGGCGGAGCTATTTACGCT 942
66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                28 ThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
                                                                                                                                                                                                                                                                                                                       8 AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer 27
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                                                                                                         GlyValAlaProLeuValAspAsnAspGluThr-----ValLysAlaLeuAlaSerLys 65
                                                          CCTGTAGTTACCCTAGTGGATAATGGCCCTACCTACTTATAAACAATATCGCCAATAAT 1002
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28 ThrSerGinValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47  28 Sizizi	ignment Scor ed. No.: orcent Simila rcent Simila st Local Sin ery Match: :	IGIUALA 161          GAAGCT 1272	ON LIELENSPILIGIALAGIAPHELEUTHTTHASAGIATTATATATGVALLEUVALALA 105    1048 TCTGCCGACCGCCATGCTATTATTTTTAATGAAAATATTGTGACTAATGCA 1107    1048 TCTGCCGACCGCCATGCTATTATTTTTAATGAAAATATTGTGACTAATGCA 1107    105	1003 AAGGGGGGCGCTATCTATATAGACGGAACCAGTAACTCCAAAATT
Qy  48 GlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLys 65	Pred. No.:  0.826  Description:  10.806  Matches:  39  Percent Similarity:  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.888  10.8888  10.888  10.888	PATENTE 103, APPLICALION US/09358// PATENT NO. 6432916 GENERAL INFORMATION: APPLICANT: Brobst, Peter APPLICANT: Bhatia, Ajay APPLICANT: Skeiky, Yasir APPLICANT: Filing, Steve APPLICANT: Maisonneuve, Jeff TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C5 CURRENT APPLICATION NUMBER: US/09/556,877 CURRENT APPLICATION NUMBER: US/09/556,877 CURRENT FILING DATE: 2000-04-19 NUMBER OF SEQ ID NOS: 305 SOFTWARE: FastSEQ for Windows Version 3.0/4.0 LENGTH: 2934 TYPE: DNA ORGANISM: Chlamydia US-09-556-877-183 Alignment Scores:	'alAlaValArga: :::    :::    :::   :::    :::    :::    :::    :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::  :::   :::   :::   :::   :::   :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!!  ::::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  :::!  ::	Db 1108 AATGGTACCAGTACGTCAGCTAATCCTCCTAGAAGAAATGCA 1149

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APPLICANT: Steven P. Fling
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
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                                                                                                                                                                                                                                  1147 AATGGTACCAGTACGTCAGCTAATCCTCCT------
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                                                                                                                                                                                                                                                                      106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                925 ---GGTAGGATCTTTTTAGTGACAATATCACAAAAAATTATGGCGGAGCTATTTACGCT 981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 ThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer 27
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                  ThrAsnGluGluAla 161
                                                          ATTTTTATGATCCTATTGAAGTTAGCAATGCAGGG------GTCTCTGTGTCC 1296
                                                                                                                                              ATAACAGTAGCAAGCTCCTCTGGTGAAATTCTATTAGGAGCAGGGAGTAGCCAAAATTTA 1248
                                                                                                                                                                                    ValAlaValArgAsn-----TyrLeuLeuGlyLysGlyIleAsnGln-----
                                                                                                                                                                                                                                                                                                                        TCTGCCGACCGCCATGCTATTATTTTAATGAAAATATTGTGACTAATGTAACTAATGCA 1146
                                                                                                                                                                                                                                                                                                                                                                IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
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                                                                                                 -----AlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly 156
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, Shuang-yong For Construction of Thermus-E. coli Shuttle TITLE OF INVENTION: Method For Construction of Two Thermus Plasmid TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid TITLE OF INVENTION: Replication Origins FILE REPERENCE: Thermus Shuttle Vector CURRENT APPLICATION NUMBER: US/09/134,246B CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ. ID NOS: 30
                    Sequence 1, Application US/09036987A
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                                                                                                                                                                                                                                      120 LeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGln 139
                                                                                                                                                     140 AlaSerValGluIleIleSerPheGlyGluGluArg 151
                                                                                                                                                                                                                                                                                                                              116 TyrAsnMetSer----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AlaLeuAlaSerLysLeu-------ProSerLeuValTyrPheAspPheAspSer 76
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
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MEDIUM TYPE: Floppy
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CITY: Indianapolis
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 28
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6014 ATGGGCAGGATAGAAGCTGACCGTTGTCAGGTCGCCGAAGGTTCCGGTCAGCCGTCCCCG 6073
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                                     AspGluArg-----
                                                               GATGCGAGCCAATTCCAGGCTGCCGGTCAACACGCAGCCACCCTCGCCGCTGGTGATGTG 6013
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Treadway, Patti J.
Turner, Jan R.
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Crawford, Kathryn P.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/370,700 CURRENT FILING DATE: 1999-08-09 EARLIER APPLICATION NUMBER: US 09/36987 EARLIER FILING DATE: 1998-03-09 NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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6074 GTAGGTGGATCCCACCGCATCACAGTTGTCTTCGACGAGGAACAGCTCGTGTTCTTTGC 613:
                                                                                                                                                                                                                                                                                                                                                                                                                           5864 ACCGAGGTGGTAGTCGAACCTCTTGCG------GCAGGTGTTGTCCACGCCGGG
                                                                                  6014 ATGGGCAGGATAGAAGCTGACCGTTGTCAGGTCGCCGAAGGTTCCGGTCAGCCGTCCCCG 6073
                                                                                                                                                                   5954 GATGCGAGCCAATTCCAGGCTGCCGGTCAACACGCAGCCACCCTCGCCGCTGGTGATGTG
                                                                                                                                                                                                                                                                                                                                           5912 CTCGCACCAGCAATCCCGTCCCCAGTCACGCAGCGA----
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                                      112 -----GlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal-----
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                                                                                                                                                                                                         89 GluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThr 108
                                                                                                                                                                                                                                                                                                                                                                              49 ValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSer
                                                                                                                                                                                                                                                                                              69 LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 SerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGly 48
                                                                                                                               AspGluArg----
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Turner, Jan R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSer 146
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RESULT 38
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                     3915170 GCGATGACGGCCGATGTCTTC---GGCGCCGCACCCGATGTCGAAGCGGGCCAGATCGAC 3915114
                   3914957 CTGGGATCCCACCGAGCTCACCGCGACGCTGCGGGACTACTTTGCTGGTCGGGATCCGGA 3914898
                                                                                                             3915014 GTGACGCTGGTGTCACCGCCGCACATGGAGCGCCGGTTCAGCGCGGAC---GGCACGTCG 3914958
                                                                                                                                                                                                          3915071 GCGTCCCCGGCTGCCGCGAAGTCAACGGTCAGGTG---TTCATCGTCTACGGTCCGCAG 3915015
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                                                                                                                                                          AlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSer 119
                                                                                                                                                                                                                                                                                                         CCGCTGTCGCCGCAGCATGTGGTAAGCCTGGTCCAGTTT----
                                                                                                                                                                                                                                                                                                                                                   LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrVal 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThr 39
                                               LeuGlyGluArgArgAla-ValAla---ValArgAsnTyrLeuLeuGlyLysGlyIleAs 138
                                                                                                                                                                                                                                                         LysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThr 99
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Sequence 79, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                        Query Match:
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35256 GGACTGGTGATGCTGGGGGCTGCAGCATGGTACACGCTGTACCAGAATCAGGAGCAGGCC 35315
                                                                                                                                                                                        35145 CTGAACAGAAATATTGCTGCCAGAAGCGCCCCAGAATGCGCTGAACAGTACAACGGCG 35204
                                                                                            35205 GTGGGCTCACGTCTGATGAGCGGTGCGCTG------GGGCTGGTTGGTGGCGTACCC 35255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-Dec-1999 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: mEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                          43 GlyValIleTyrThrGlyValAla------ProLeuValAspAsnAspGlu-----
                                                                                                                                         23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
                                                                                                                                                                                                                                     3 LeuHisIleGlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly 22
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ZIP: 53701-2113
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REFERENCE/DOCKET NUMBER: 960296.95017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/453,702B
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Alignment Scores:
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Sequence 137, Application US/09453702B

Patent No. 6365723

GENERAL INFORMATION:
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                                                                                                                                                                     TELEPHONE: (608) 251-910
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELEPHONE: (608) 251-5000
TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/09/453,702B
FILING DATE: 03-DEC-1999
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
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ADDRESSEE: Quaries & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35499 CAGGATGTGCTTGCCGGGCTG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35448 GATGAACAGGCCAGTCGGGTGAAATCCCTG------CAGGAAAAAGCGCAGTCCATT 35498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35430 GAGCAGAACCGGCTGATT----- 35447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35376 ATGTCTTTGCCTGAAGCCTCAGATAATGAAGGACGAACACGGGCGCG-----CTGACA 35429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35316 AGGGAGTCTGCGCGCCAGTATGCACTGACGATAGATGAAATCGCGCATAAAACGCCGTCA 35375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 GluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 AspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 GluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp 88
                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                           LENGTH: 48908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: WI
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Darna, Nicole T.
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Welch, Rod
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Soon

Search completed: July 6, 2003, 13:40:31 Job time: 1768 secs

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=x1p
-Y-C9T2_1/USPFO_spool/US99674779/runat_06072003_121615_9891/app_query.fasta_1.327
-DB=Published_Applications_NA -QEMT-fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-THR.MS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0
-MAXLEN=2000000000 -USER=US09674779_@CGN_1_1_122_@runat_06072003_121615_9891
-NCPU=6 -ICPU=3 -NO_MMAP -LARGSQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-NCPU=6 -ICPU=3 -NO_MMAP -LARGSQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-CONGIGG -DEV_TIMEOUT=120 -WANT -MATRIX-DISTORES=1 -KGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                    Result
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Maximum Match 100%
Listing first 100 summaries
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1: /cgn2_6/ptodata/2/pubpna/U
2: /cgn2_6/ptodata/2/pubpna/U
3: /cgn2_6/ptodata/2/pubpna/U
3: /cgn2_6/ptodata/2/pubpna/U
4: /cgn2_6/ptodata/2/pubpna/U
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11: /cgn2_6/ptodata/2/pubpna/U
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14: /cgn2_6/ptodata/2/pubpna/U
                                                                                                                                                   Match Length DB
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-674-779B-2
861
                                                                                                                                                                                                                                                                                                                                       // cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
// cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/PCTUS.PUBCOMB.seq:*
// cgn2_6/ptodata/2/pubpna/PCTUS.PUBCOMB.seq:*
// cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
// cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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10 US-09-747-348-1
19 US-10-329-960-1
9 US-10-216-338A-5
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1931.586 Million cell updates/sec
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US-10-329-960-1/c
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CURRENT EILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR EILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fraç
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
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                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/747,348
CURRENT FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/171,525
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and FILE REFERENCE: 77813-37
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                      LENGTH: 779
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                     NAME/KEY: CDS
LOCATION: (10
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PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
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LOCATION: (10150)..(10150)
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (36636)..(36
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LOCATION: (47036)..(47036)
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LOCATION: (45732)..(45732)
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals
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LOCATION: (51334)..(51334)
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NAME/KEY: misc_feature
LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals
                                                      NAME/KEY: misc_feature
LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (65313)...(65313)
OTHER INFORMATION: n equals
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LOCATION: (65309)...(65309)
OTHER INFORMATION: n equals
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LOCATION: (145171)..(145171)
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LOCATION: (145058)..(145058)
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LOCATION: (131360)..(131360)
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LOCATION: (140398)..(140398)
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LOCATION: (139910)..(139910)
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LOCATION: (131340)..(131340)
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LOCATION: (122336)..(122336)
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LOCATION: (142750)..(142750)
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LOCATION: (121344)..(121344)
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LOCATION: (107248)..(107248)
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LOCATION: (117136)..(117136)
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LOCATION: (119924)..(119924)
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LOCATION: (119750)..(119750)
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LENGTH: 984
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                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10216338A Publication No. US20030113757A1 GENERAL INFORMATION:
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                                                                                                  CURRENT APPLICATION NUMBER: US/10/216,338A CURRENT FILING DATE: 2003-01-14 PRIOR APPLICATION NUMBER: 60/310,882 PRIOR FILING DATE: 2001-08-08 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                 APPLICANT: Czajka, John
TITLE OF INVENTION: Rapid and Specific Detection of Campylobacter
FILE REFERENCE: MD1083USNA
                                                                                      SOFTWARE: Microsoft Office 97
ORGANISM: Campylobacter coli
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LOCATION: (152530)..(152530)
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR ETLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3232
LENGTH: 678
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Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
                                                                                                           Alignment Scores:
                                                                                                                                           ; LOCATION: (1).
US-10-156-761-3232
                                                    Percent Similarity:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
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                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Streptomyces avermitilis
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SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10156761 Publication No. US20030119018A1
                                                                                SEQ ID NO
                                                                                                                      CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                     APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                        APPLICANT: APPLICANT:
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                                                                                                    NUMBER OF SEQ ID NOS: 15109
                 ORGANISM: Streptomyces avermitilis
FEATURE:
                                          TYPE: DNA
                                                            LENGTH:
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HORIKAWA, HIROSHI
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US-10-216-338A-7
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                                                                                                                                                                                  Sequence 7, Application US/10216338A Publication No. US20030113757A1 GENERAL INFORMATION:
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                                        CURRENT APPLICATION NUMBER: US/10/216,338A
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: 60/310,882
PRIOR FILING DATE: 2001-08-08
                                                                                                                       TITLE OF INVENTION: Rapid and Specific Detection FILE REFERENCE: MD1083USNA
                                                                                                                                                                 APPLICANT: Czajka, John
    SOFTWARE: Microsoft Office 97
                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c,
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US-09-674-779B-2 (1-172) x US-09-452-599-11 (1-730)
                                                                 Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                     ; SOFTWARE: Pat
; SEQ ID NO 11
; LENGTH: 730
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Best Local Similarity:
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LENGTH: 861
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Roy, Paul H.
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US-09-674-779B-2 (1-172) x US-10-216-338A-7 (1-861)
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FILE REFERENCE: 12287.31
CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1994-09-12
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
NUMBER OF SEQ ID NOS: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               814 GAAAAAAGTCGCATCAAAACAGTAGGTTATGGTCAAGATAATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 MetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIle 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 ValLysAlaLeuAlaSerLysLeuProSerLeuVal---TyrPheAspPheAspSerAsp 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro 152
                      Indels:
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; OTHER INFORMATION: P40 US-10-169-953-1
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US-10-169-953-1
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Best Local Similarity:
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DB:
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Publication No. US20030044915A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT FILE REFERENCE: D18390
CURRENT APPLICATION NUMBER: US/10/169,953
CURRENT FILING DATE: 2002-07-03
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LOCATION: (1)..(1032)
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                                                                                                                             643 CTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAG
104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
                                         703 GCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTT
                                                                               86 IleLeuAspGluGlnAlaGlnPheLeuThrThr-----AsnGlnThrAlaArgValLeu 103
                                                                                                                                                                  66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
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           RESULT 11
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHIGENOBU, SHUJI APPLICANT: WATANABE, HIDEMI
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TYPE: DNA
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                                                      365166 TATCCGTTA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 IleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGlu-----
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                                                                                             ArgProIleAlaPheGlyThrAsnGlu 159
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                                                           ----ACTAATCAA 365149
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Best Local Similarity:
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                                                                                                                                    Sequence 25, Application US/09998279 Publication No. US20030083287A1 GENERAL INFORMATION:
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                                  APPLICANT: BURGESS, NICOLA A.
APPLICANT: GARCIA, MIGUES M.
APPLICANT: KIRKE, DAVID F.
APPLICANT: MEYERS, NICHOLAS L.
APPLICANT: WILLIAMS, PAUL
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LENGTH: 561
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FILE REFERENCE: GM50081
                   TITLE OF INVENTION:
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CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR ETLING DATE: 2000-10-06
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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
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NUMBER OF SEQ ID NOS: 8481
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                                                                                                                                                                                                                                                                                                                                                                                                                  390 ATGGGGCTTTTAATCGAAAATCCAAAGCTTGACGCCAAGATCTTCAGCGCGAAAGGCTAC 449
                                                                                                                                                                                                                                                                                                        168 AlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerVal---GluIleIleSerPhe 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 ---ArgGlySerArg----GluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 AspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGln 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 ValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPhe 72
                                                                                                                                                                                                                                                                                                                                    GGGGAATTTAAACCGATCGCTTCAAATGACACCGAAGAAGAAGAAGAAGAAAAACAGACGC 509
                                                                                                                                                                                                                                                                                                                                                                           GlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCGAAATTCTCAATTTAAATCAAATTGGCATTTAAGCGTGATGCGGGCTGTCAATTTC 389
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; ORGANISM: Bacillus licheniformis US-09-974-300-1889
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US-09-974-300-1889
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APPLICANT: Berka, Randy M.

APPLICANT: Clausen, Ib Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

CURRENT FILING DATE: 2001-10-05
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                                                                            NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1889
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1889, Application US/09974300 Patent No. US20020146721A1
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LENGTH: 1143
                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06
                                          TYPE: DNA
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CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,288
PRIOR FILING DATE: 2000-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      856 AATAGTGCAAAGATTGATCGTAATCAAGAAATCAATGTTTACAATACAGCTGAATATGCG
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US-10-010-160-11
; Sequence 11, Application US/10010160
; Publication No. US20030103999A1
                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (1)...(714)
US-10-010-160-11
                                                                              Alignment Scores:
                                                         Pred. No.:
Best Local Similarity:
                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 717
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/010,160
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: AU PRI381
PRIOR FILING DATE: 2000-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR TITLE OF INVENTION: TREATING INFECTION BY LAWSONIA SPIFILE REFERENCE: DAVIIIO.001AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Good, Robert T, APPLICANT: King, Kendall W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosey, Everett L.
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/249,596 PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                   ORGANISM: Lawsonia intracellularis
                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyr------AsnMetSer 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 CTCGTCCTTCAGGAAGCGGTTTTGTTTGATTCAGGGAAAGCGGATCTGAAAGACCAAGCT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              624 GAGAGCCATATGAAGGAAAACAGGCGCGTCGAGATT 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 TCGTCGCGTTTTCTTGCCATCGGTTATGCGGATACAAAACCGGTCAGGGACAACCGCACT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 AlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeu 103
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11.79%
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42.21%
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                     Conservative:
                                            Matches:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
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                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                     ATTORNEY/AGENT INFORMATION:
                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                           STREET:
                                        CLASSIFICATION: 435435
                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                               COUNTRY:
  NAME:
                                                          FILING DATE:
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US20020119447A1
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POREMBSKI, PRISCILLA E.
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GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                               100 ABBOTT PARK ROAD
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SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                   USA
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TAMI J. PILOT-MATIAS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08424550B Patent No. US20020119447A1
                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              APPLICANT:
                                       CORRESPONDENCE ADDRESS:
                                                                        TITLE OF INVENTION:
                                                                                                             APPLICANT:
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                                                        NUMBER OF SEQUENCES:
                                                                                                                                               APPLICANT:
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No.:
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STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: DNA ()
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REFERENCE/DOCKET NUMBER: 55:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4268 base pairs
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                                                           THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
VENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEDATITIS
VENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                             GEORGE J. DAWSON
GEORGE G. SCHLAUDER
                                                                                                                                                                                                                                            TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                              JOHN N. SIMONS
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; Sequence 390, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
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                                                                                            RESULT 17
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TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 11:
APPLICANT:
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No.:
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REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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NAME: POREMBSKI, PRISCILLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: SOFTWARE: PatentI
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                                                                                                                         5226 CATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGC 5267
                                                                                                                                                                                             5169 ---ACTAGTCCTTTCACATTGGAAACCGCCCTTGAAAAACTTAACACCTTTCTTGGGCCT 5225
                                                                                                                                                                                                                                                                            5130 GTTGCTGCAATT---GACAAGCTGAAGAGTACAATCACCACA-----
                                                                                                                                                                                                                                                                                                                                                               5103 GCATCATTCATTCCC-----
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                                                                                                                                                         123 ArgArgAla-----ValAlaValArgAsnTyrLeuLeuGly 134
                                                                                                                                                                                                                                  103 LeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGlu 122
                                                                                                                                                                                                                                                                                                             83 AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
                                                                                                                                                                                                                                                                                                                                                                                     63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60064-3500
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JOHN N. SIMONS
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Matches:
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INFORMATION FOR SEQ ID NO: 390:
SEQUENCE CHARACTERISTICS:
LENGTH: 9143 base pairs
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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TOR-938-2623
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TOPOLOGY: li
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5318 GTTGCTGCAATC---GATAAGCTGAAGAGTACAATAACCACA----
                                                                               5291 GCATCATTCATTCCC-----
                                     83 AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
                                                                                                                 63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGln 82
                                                                                                                                                                                              43 GlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeu 62
                                                                                                                                                                                                                                                                              23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
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SHERI L. BUIJK
ISA K. MUSHAHWAR
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THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
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GEORGE G. SCHLAUDER
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Best Local Similarity:
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                                                                                                                                               Alignment Scores
                                                                                                                                                                                                                    US-08-424-550B-393
                                     Percent Similarity:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-B. NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                              FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                               NAME/KEY:
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GEORGE G. SCHLAUDER
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TAMI J. PILOT-MATIAS
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                                                                                     US-09-674-779B-2 (1-172) x US-09-742-659-1 (1-9399)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                   ; LENGTH: 9399
; TYPE: DNA
; ORGANISM: GB virus-B
US-09-742-659-1
                                                                                                                                                            Query Match:
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                                                                                                                                                                                                                                                           Alignment Scores:
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US-09-742-659-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ID01116
CURRENT APPLICATION NUMBER: US/09/742,659
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/171,469
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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  5141 CTCGCTGTTGGCGTTGGAGTGGCTATGGCTTATCTAGCCATTGACACTTTTTGGCGCCCACT 5200
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                                        3 LeuHisIleGlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
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; SEQUENCE DESCRIPTION: SEQ ID NO: 121: US-09-070-927A-121
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                                                                                                               INFORMATION FOR SEQ ID NO: 121: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-11-14 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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Patrick J. Dillon
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                                                       LENGTH: 8033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                        TOPOLOGY: linear
                                                                                                                                                                                                              NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERAVING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Maryland
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US-09-886-468-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09886468 Patent No. US20020037293A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Aventis Pasteur Limited TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses ther FILE REFERENCE: 77813-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/113,280 PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/886,468
CURRENT FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/113,283 PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/113,282
PRIOR FILING DATE: 1998-12-23
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PRIOR FILING DATE: 1998-12-23
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                                                                                                                                                                                             APPLICATION NUMBER: 60/114,050 FILING DATE: 1998-12-28
                                                                                                                                                                                                                                                                                  FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/113,285
FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/113,284 FILING DATE: 1998-12-23
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                                                                                                   APPLICATION NUMBER: 60/114,057 FILING DATE: 1998-12-28
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FILING DATE: 1998-12-28
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APPLICATION
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LOCATION: (101)..(2713)
US-09-886-468-8
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Best Local Similarity:
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SEQ ID NO 8
LENGTH: 2816
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                    Sequence 486, Application US/09841132 Patent No. US20020061848A1
                                           APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILIG DATE: 2001-04-23
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         NUMBER OF SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Chlamydia pneumoniae
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         SEQ ID NOS: 599
FastSEQ for Windows Version 3.0/4.0
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SEQ ID NO 486

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; TYPE: DNA; Chlamydia US-09-841-132-171
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                                                       SEQ ID NO 171
LENGTH: 2895
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                                                                                                                                                                                                                                                                                                                  Sequence 171, Application US/09841132 Patent No. US20020061848A1
                                                                                                                                                                 APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
                                                                                                              CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 SerValLeuThrPheMet---------ThrGlyCysAlaAsnLys 26
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Best Local Similarity:
                                                                                                                                          ; LENGTH: 2934
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-183
  Query Match:
                                           Percent Similarity:
                                                                Score:
                                                                                    Pred. No.:
                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-841-132-183

; Sequence 183, Application US/09841132

; Patent No. US20020061848A1
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APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46968
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILLING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 183
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                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1003 AAGGGGGGCCTATCTATATAGACGGAACCAGTAAC-----TCCAAAATT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 ThrAsnGluGluAla 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 ValAlaValArgAsn------ 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     943 CCTGTAGTTACCCTAGTGGATAATGGCCCTACCTTCATAAAACAATATCGCCAATAAT 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 GlyValAlaProLeuValAspAsnAspGluThr-----ValLysAlaLeuAlaSerLys 65
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23.64%
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               Mismatches:
                                Conservative:
Indels:
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US-09-674-779B-2 (1-172) x US-09-841-132-183 (1-2934)
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                                                                                                 US-09-674-779B-2 (1-172) x US-10-007-693-58 (1-1086)
                                                                                                                                                                                     Percent Similarity: Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/10007693 Patent No. US20020146776A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/007,693 CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECT:
FILE REFERENCE: 210121.515C2
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1086
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         472 AGTGCTCTTCACAATGTGCTCTTTCCTCTTGGGGAAATGAATAAGACTGAAGTTCGTGCG 531
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                                                   12 AlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSerGlnVal 31
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                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1).
US-10-156-761-1993
                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1993, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1993
LENGTH: 1260
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             646 GGCAACGTTATC-----GATTGGGATACCAAGGAAATTGTAGGGCAA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            793 ATTTATATTGTGAGG----GGGGAAGACCATCCC 822
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                                         514 GAGATCGCGGCCAAGGGCGTCGGGCTCACCATCGACACCCTCGGTCTGGTGCCGAACAGC 573
26 LysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIle 45
                                                                                   6 GlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn
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HORIKAWA, HIROSHI
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Query Match:
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                                       Best Local Similarity:
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US-10-156-761-1
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LENGTH: 9025608
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Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR ETLING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: JP 2001-272897 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORKKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                    ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6221, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Clausen, ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                         LENGTH: 315
TYPE: DNA
ORGANISM: Bacillus clausii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AGCGCCCGCGCTTACAATGTCATGAAACTGTTTTTCGAATACGATCATTTTGAGCCGGCT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GluArgArgAlaValAlaVal---ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAla 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 SerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 CAACTGTCATTTGCAGGCTACGGTGAGTATCATCCGATCGCTTCAAACGAGACTGCAGAA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GGAAGGCAAGCCAACCGACGCGTTGAAGTC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 AlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 CTAATCGAGCAACTATCGGCTATGCTTGCTTGACCCACCGCGCTATATTCAAATTTCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                                                                     333 ---GGTAGGATCTTTTTAGTGACAATATCACAAAAAATTATGGCGGAGCTATTTACGCT 277
                                                                                                                                                                                                                                                                                                                                        390 GCTTCTGATGGAGGAGCAATTAAAGTAACTACTCGCCTAGATGTTACAGGCAATCGT--- 334
                                                                                  216 AAGGGGGGCCCTATCTATATAGACGGAACCAGTAAC------TCCAAAATT 172
                                                                                                                                                                   276 CCTGTAGTTACCCTAGTGGATAATGGCCCTACCTTATAAACAATATCGCCAATAAT 217
171 TCTGCCGACCGCCATGCTATTATTTTTAATGAAAATATTGTGACTAATGTAACTAATGCA 112
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                                                                                                                                                                                                             48 GlyValAlaProLeuValAspAsnAspGluThr-----ValLysAlaLeuAlaSerLys 65
                                                                                                                                                                                                                                                                                             28 ThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
                                        86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                          66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                                                                                                                                                                                8 AlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer 27
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US-10-062-254-323/c
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PRIOR FILING DATE: 2000-07-28
PRIOR PELLOATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR APPLICATION NUMBER: 60/156099
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/157287
PRIOR APPLICATION NUMBER: 60/157287
PRIOR APPLICATION NUMBER: 60/157287
                                                                US-09-674-779B-2 (1-172) x US-10-062-254-323 (1-1762)
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                                                                                                                       Query Match:
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Best Local Similarity:
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Patent No. US20020138882A1
                                                                                                                                                                                                                                                                                                                       SEQ ID NO 323
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CURRENT FILING DATE: 2002-02-01
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PRIOR APPLICATION NUMBER: 60,
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Office 97
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PRIOR APPLICATION NUMBER: 60/
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                                  4 HisīleGlnīleAlaAlaAlaAlaAla------AlaLeuSerValLeuThrPheMet 20
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Falco, Saverio Carl
Fang, Yiwen
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US-09-674-779B-2 (1-172) x US-10-156-761-6208 (1-2631)
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                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 eAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 TGGGGGTTTGGATGGAAGGGAATCGATCGAT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 CGATTCCGGAACGTCGCGCTCTCGCACCGAACCTCGACCGCCGCCACTGTCGTATTTTGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 ArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg-AsnTyrLeuLe 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GCCGTCACACAGCGATATCTCGATGTCCTCCGCGTGGCTCACCGACATCTTCGCCGCCGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 ---GATAGCCTTCCGCCGCAGCGAGCCGATCTTACGCCGCCGCCGCCGCTCGTCCTCCGAGTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 GAAGCGGAAGTCGACGCGGCGCCTCCCTCGCTTCTTGAGCGCGTG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 LeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySer 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 SerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGln-----AlaGlnPhe 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 TGGTAGTCGTCGTGCTTGTCGGG-GAGGAGGCGGTGCGCGGCGAGGCGGTCCCGGAAGGA 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 TyrThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAsp------ 56
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
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                                                                                               PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                       PRIOR PRIOR
                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                  PRIOR
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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APPLICATION NUMBER: 60/257,931
                     APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 GlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIle 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   922 GGACTGGCGCGGGAGCCACGTGTGGATCACGCGCGCGGGCTGAGCGCCCTGACGACGGTA 981
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                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                     Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                        Trawick, John D.
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                                                            2000-10-23
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RESULT 31 US-10-156-761-6208

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

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; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)... US-10-156-761-6208

SEQ ID NO 6208 LENGTH: 2631

TYPE: DNA

Query Match:

Best Local Similarity: Percent Similarity: Pred. No.: Alignment Scores:

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; NAME/KEY: CDS
; LOCATION: (1).
US-09-815-242-9978
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9978
LENGTH: 1317
                                                                                                                                   US-09-919-039-60
                                                                                                                                                      RESULT 33
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                    GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
                                                                                           Sequence 60, Application US/09919039 Publication No. US20030108871A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Salmonella typhi FEATURE:
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                TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 ----
                                                                                                                                                                                                                                                                                                          143 GluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrp 162
                                                                                                                                                                                                                                                                                                                                                   595 AAACTGCGCGTCTACGAGAAGGCGAAAGTGTGCGTAGTGAATGCCGATGACGCGTTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 ProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIle 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu
                                                                                                                                                                                              715 CACCTTAATCGTCAG 729
                                                                                                                                                                                                                                   163 SerGlnAsnArgArg 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                HisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGly 106
                                                                                                                                                                                                                                                                       ATGCCGGTACGCGGGCCGATGAGCGCTGCGTCAGCTTTGGCGTCAATATGGGTGATTAT 714
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US-09-919-039-60
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PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 60
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                                 US-09-674-779B-2 (1-172) x US-09-960-253-145 (1-10300)
                                                                                                                                                                               Alignment Scores:
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                                                                                      Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 145, Application US/09960253 Patent No. US20020123619A1
                                                                                                                                                                                                                                                                                        SEQ ID NO 145
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mohamath, Raodoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.556
CURRENT APPLICATION NUMBER: US/09/960,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Incyte ID No. US20030108871A1 348072.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Benson, Darin R.
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 187
                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE:
                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                               No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu 110
59 ValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGlu 78
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Indels:
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roThrGlyTyrThrGlyValIleTyr    	US-09-674-779B-2 (1-172) x US-10-156-761-5966 (1-465)  QY 7 IleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys 26  :::	Percent Similarity: 38.65% Conservative: 25 Best Local Similarity: 23.31% Mismatches: 55 Query Match: 8.77% Indels: 45 DB: 9 Gaps: 7	Length: Matches:	; NAME/KEY: CDS ; NAME/KEY: CDS ; LOCATION: (1)(465) US-10-156-761-5966	; LENGTH: 465 ; TYPB: DNA ; ORGANISM: Streptomyces avermitilis	ro.	9 9 9 9	FILE FOR INVESTIGATION NUMBER: US/10/156,761	₹	ISHIKAW HORIKAW SHIBA,	- 0	RESULT 35 US-10-156-761-5966 ; Sequence 5966, Application US/10156761 ; Publication No. US2003011901881	GCTCTACAGGAAGAG	Qy 161 AlaTrpSerGlnAsnArgArgAla 168	QY 141 SerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu 160	Qy 121 GlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAla 140	Qy 105 AlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSer:Leu 120  Db 217 GACCCTGAATTACACCAAGAATCTGACATGGAATTTAATACTACACAAGAAGATGTT 276	QY       95	97 CTGGAGCCTCAGGCGGCTTCTAGAAATGCTGAGCCGATTATCAGGATTAGCAAAT		Db 37 GTGGAAGGTGTCGCGTACGGGCTTCCCGAGCTGACGTGGCTTGAATTGGGAGGGGGGCAG 96
Alignment Scores:  Pred. No.:  2.88  Score:  75.50  Matches:  Percent Similarity:  38.75%  Conservative:  24	; LENGTH: 2382 ; LENGTH: 2382 ; TYPE: DNA ; ORGANISM: Staphylococcus aureus US-09-815-242-4642	PLICATION   LING DATE: F SEQ ID NO: F FASTSEQ	APPLICATION   FILING DATE: APPLICATION	; PRIOR APPLICATION NUMBER: 60/207,727 ; PRIOR FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: 60/242,578 ; PRIOR FILING DATE: 2000-10-23		FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191.078	; APPLICANT: Xu, H. Howard ; TITLE OF INVENTION: Identification of Essential Genes in ; TITLE OF INVENTION: Prokaryotes	; APPLICANT: Trawick, John D. ; APPLICANT: Carr, Grant J. ; APPLICANT: Yamamoto, Robert T.		NFOR	RESULY 36   US-09-815-242-4642   Sequence 4642, Application US/09815242	388 GGAACTTCG	Oy 161 AlaTrpSer 163	147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu	Oy 127 AlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSer 146	Qy 107 HisthraspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal 126 :::             :::	8/ LeuAspGiuGinAlaGinPheLeuThrThrAsnGinThrAlaArgValLeuValAlaGiy	154AAGTGCAAGCCCGACATCCAGACGGAC	ProSerLeuValTyrPheAspPheAspSerAsp	47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu	

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                                                                                  PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: Fas
SEQ ID NO 8570
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                               PRIOR FILING DATE: 2001-02-16
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                  FastSEQ for Windows Version
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Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto, Robert T.
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; NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-8570
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US-10-156-761-1454/c
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                                                          APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1454, Application US/10156761 Publication No. US20030119018A1
SEQ ID NO 1454
LENGTH: 1335
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
                                          NUMBER OF SEQ ID NOS: 15109
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US-10-156-761-1454
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                                                                                                                                                                                                          Sequence 4085, Application US/09815242 Patent No. US20020061569A1
                                                                                        APPLICANT:
                                                                                                                       APPLICANT:
                        APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                    APPLICANT:
                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1104 GCTCGCGTGGGGGTCGACCCGAGTGCCGGGCCCGCGCGTCACCTGGGAGGTCACCGCCGGT 1045
                                                                                                                                                                                                                                                                                                                                        675 CGAGATGCTGTGCGGGAGGACGTCGTGCAGTTCGCGGGGCGATCCGCAGCCGCTCCTCGTC 616
                                                                                                                                                                                                                                                                                                                                                                   143 ------GluIleIleSerPhe---GlyGluGluArgProIleAlaPhe 155
                                                                                                                                                                                                                                                                                                                                                                                                   131 TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerVal------ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                               750 ----- 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1044 GTCGCCCGGGCCGTC---GTCGATCAGCACGCGCGCGTGCCGCGATCCCGAATGCCGTAC 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   927 CTTCGGCACCTCGCCCTCGATCTCGACCGT----CAACCCCGCGCTCGCCGCCTGCTCGAC 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        987 GACGTTCGTCAGTGCCTCCTGGACGATCCGGAAGGCGGCGAGATCGGTGCCGGGCGCGAG 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 Gln------ThrAlaArgValLeuValAlaGlyHisThrAspGlu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 GluGlnAlaGln-------9heLeuThrThrAsn 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 ValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuPro--- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 SerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGly 48
                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                               Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
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NUMBER OF SEQ ID NOS: 14110
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-12-22
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TYPE: DNA
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::::::||Î|Î|||||||
698 GCGTCATCGGCAAGGGCTCCCAACTGGTGGATGCCAAGGGCGACGTGGTCGCTGACGGCA 757
                                                                                                122 luArgArgAlaValAlaValArgAsnTyr-----
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US-09-674-779B-2 (1-172) x US-09-815-242-4085 (1-1707)
132 --LeuLeuGlyLysGly-----IleAsnGlnAlaSerValGluIleIleSerPheGlyG 149
                                                           638 AACAGAAGGCCGTGGCCTACGAGAGCCTGGGCGACCTCCACGACGGCGTGATGAGCGCCA 697
                                                                                                                                                                                    578 GTGGCTTGATCAGCGCCGAGCGTGGCGAGGAAGTGGATCATCAACCTCGCTACCGGCG 637
                                                                                                                                                                                                                                            108 -----ThrAspGluArgGlySerArgGluTyr-----AsnMetSerLeuGlyG 122
                                                                                                                                                                                                                                                                                                              518 AGCAGCTCACCGAGGCGCTCTACGACACCACCCTGGTCAACGGCAGCGTCGCCGAACACG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                    458 CCAACGAATTCATCATCTACGAGATCGATGGCAAGCGCGGCATCCTCGATGCCAAGGGCA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 TCGACGGCCAGGGCAAGGAAGTCCAGGCGCCGCGTTTCGACGACATCTACCCCAACAGTG 457
                                                                                                                                                                                                                                                                                                                                                                         92 lnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis------ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 AGCGCTGGAACCTGATCCAGGCGAAGGACGGCAAGGTGTTGCGCGACGATATCGGCGAAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 ACGACTACGACAATATCGTCGCCAGCGCCTACCAGGGCACCCTGATGGCGGCGCGCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 GCCTCAACGGCCAGTGCGCGGTGATCGACCAGGACGCCAAGCTGCTCGTGCCGTTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 laLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSer------ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 SerGlnValMetValAlaProAsnAlaProThr-GlyTyrThrGlyValIleTyrThrGl 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGTCGCTGCTCACCCCCAACCTCTATGGCTTCGTCCGCGATGGCAAGTACGGCGTGG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yValAlaPro-LeuValAsp------61
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LENGTH: 11575
TYPE: DNA
ORGANISM: Plasmid
US-09-938-956-5
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APPLICANT: Wang, Sigun
APPLICANT: Dicosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 5, Application US/09938956
Patent No. US20020142408A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Office 97
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
TITLE OF INVENTION: Production of Monoterpene
FILE REFERENCE: CL1809 US NA
CURRENT APPLICATION NUMBER: US/09/938,956
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/229,907 PRIOR FILING DATE: 2000-09-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10095 GCCGCGGCAGCCTTGAACGGCCTCAATTTCCTGACGGGCTGT------ 10054
                                                                                                                                                                                                                                                                                                                                                                                               10053 -----TTCCTTTTGCCGGAGTCGCACAAAGGCGAACGCCGGCCGTTACGCCGGGAGGCT 10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9879 GGCGAGGATCGCTTTCACTGGGACGCGACCACGATCGGCATTTCGCTTGCCGCATTTGGC 9820
                                                                                                                                                                                                                                                               9999 CTCAACCCGCTCGCTTCCGTTCCGGTGGGCCCGGGGCATGACCGTCGTCGCCGCCCTGATG 9940
9819 ATTCTGCATTCACTCGCCCAGGCAATGATCACCGGCCCTGTAGCCGCCCCGG------ 9769
                                                                135 LysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAla 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 ValAlaProLeuValAsp------ 61
                                                                                                                                                                                                                                                                                                                                                                                                                            30 GlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIle---TyrThrGly 48
                                                                                                                                                               95 ThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArg 114
                                                                                                                                                                                                                              75 AspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeu 94
                                                                                                                                                                                                                                                                                              62 -----LeuAlaSerLysLeuProSerLeuValTyrPheAspPhe 74
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Matches:
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Indels:
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Db 9678 TTC 9676

Search completed: July 6, 2003, 15:04:07
Job time: 3796 secs
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Command line parameters:

-MODEL-frame+_P2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US99674779/runat_06072003_121613_9801/app_query.fasta_1.327
-DB=GenEmbl -QFMT_fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DB-GenEmbl -QFMT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=100
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-QUERMT=pto -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09674779_@CGN_1_1_1319_@runat_06072003_121613_9801 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 100 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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861
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

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Sequence 1 from Patent W09957277.
AX011034
                    antibodies, and uses
Patent: WO 9957277-A 1 11-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHAM
                                                                                                                                   AX011034.1 GI:9997679
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Location/Qualifiers
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U75869 Helicobacte
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AE002355 Chlamydia
AE001335 Chlamydia
AF117972 Pseudomon
D78346 Rickettsia
AE012192 Xanthomon
AF117975 Pseudomon
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AL591783 Sinorhizo
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AR199522 Sequence
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Sequence 36 from Patent W00078968.
AX067461
                                                                             Lagace, R.E., Patterson, C. and Berg, K.L.
Nucleotide seguences of moraxella catherhalis
Patent: WO,0078968-A 36 28-DEC-2000;
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                                                               Incyte Genomics, Inc. (US)
Location/Qualifiers
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LOCUS

KEYWORDS SOURCE

Moraxella

ORGANISM

Bacteria; Moraxella

Moraxella

VERSION

REFERENCE

AUTHORS

Ruelle, J.L. Basb019 pro

TITLE

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Alignment Scores: Pred. No.:
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                                                                                                  antibodis, and uses
Patent: WO 9957277-A 3 11-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE |
Location/Qualifiers
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Moraxella catarrhalis
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AX011036
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                                                                        /db_xref="taxon:480"
                                                                                  /organism="Moraxella catarrhalis"
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US-09-674-779B-2 (1-172) x AX011036 (1-519)
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                                                                                                                           /organism="Moraxella catarrhalis"
/db_xref="taxon:480"
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Sequence 7 from Patent WO9957277,
AX011040
                                                                                                                                                                                              antibodies, and uses
Patent: WO 9957277-A 7 11-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE
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                                                                                                                                                                              Location/Qualifiers
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/db_xref="taxon:480"
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Characterization of an OprL null mutant of Pseudomonas
J. Bacteriol. 178 (19), 5836-5840 (1996)
                                                                                                                                                                                                                                                             Rodriguez-Herva, J.J., Ramos-Gonzalez, M.I. and Ramos, J.L. The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                 oprI gene; tolA gene; tolB gene; tolR gene.
Pseudomonas putida.
Pseudomonas putida
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                       Direct Submission
Submitted (21-JUL-1993) I. Ramos-Gonzalez,
del Zaidin, 18008 Granada, SPAIN
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Submitted (09-JUN-1995) I.
                Direct Submission
                           Ramos-Gonzalez,I.
                                                                                                Ramos-Gonzalez,
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     Ramos-Gonzalez,
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        C.S.I.C. Estacion Exper
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                                                                             Estacion Exper.
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jul 17,
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5 (bases 1 to 7577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5075 GAGCGTCGTGCGAAAGCCGTTCAGCGCTACCTGGTTCTGCAGGGCGTTTCCCCTGCTCAG 5134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                 162 TrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysPro 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 ThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAla 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 LysSerThrSerGln-------ValMetValAlaProAsnAlaProThrGlyTyr 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn
                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                             P.aeruginosa oprL gene
                                                                                                                             outer-membrane peptidoglycan-associated lipoprotein (PAL)
                                                                                                                                                                         Lim, A. Jr., De Vos, D., Brauns, M., Mossialos, D., Gaballa, A., Qing, D.
                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                  oprL gene; outer membrane protein
                                                                                                                                                                                                                                                                                                                            PAOPRLGN
Submitted (12-MAR-1997) Lim A., Vrije Universiteit Brussel, Paardenstraat 65, St. Genesius Rode, Belgium
                             Direct Submission
                                                                                                  Pseudomonas aeruginosa
Microbiology 143 (Pt 5), 1709-1716 (1997)
                                                                                                                                              Molecular and immunological characterization of OprL,
                                                                                                                                                           and Cornelis, P.
                                                                                                                                                                                                          Pseudomonas.
                                                                                                                                                                                                                                                                                Z50191.1 GI:2251191
                                               Lim, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAla 161
                                                                                                                                                                                                                                                                                                                                                                                     TGGGCTCAGAACCGTCGCGTAGAACTG 5221
                                                          (bases 1 to 1048)
                                                                                                                                                                                         (bases 1 to 1045)
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3 (bases 1 to 1048)
                                                                                                                                                                              Similarity:
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                                                                                                                                                                                                                                                                                  195
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212. .718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="unknown"
/protein_id="CAA90571.1"
/db_xref="GI:929775"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="orf3"
728. .>1048
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                                                                                                                                                                                                                                                                                                CNPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                     /product="periplasmic protein"
/protein_id="CAA90572.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="orf3"
                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:Q51490"
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Matches:
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Submitted (01-AUG-1995) Lim A., Vrije Universiteit Brussel, Faardenstraat 65, St. Genesius Rode, Belgium On Jul 9, 1997 this sequence version replaced gi:929774.

Location/Qualifiers
                                                                        233 AAATTTGCTGCGCTGGCTCTGGCCATGGCTGTG------GCTGTGGGGTTGCTCCTCC
      26 Lys-----SerThrSerGlnValMetValAlaProAsnAlaProThr
                                                                                                                                   6 GlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="homology with TolB of E.coli and Haemophilus
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/db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="memlkfgkfaalalamavavgcsskggdasgeganggvdpnagy
Gansgavdgslsdeaalraittfyfeydssdlkpeamraldyhakdlkgsgorvvleg
HTDERGTREYNMALGERRAKAVQRYLVLQGVSPATLELVSYGKERPVATGHDEQSWAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="outer membrane protein"
/protein_id="CAA90573.1"
/db_xref="01:2251192"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="SPSVAPNGTMLIRHPPAGPGVLMLVSSTDAYGYLSPTAQGDVRE/
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agaggaftgggvttptsvQgelfmQLQ0mQdelarlrgtlerevarmasvmQrpAgSr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 CTGGGCGAGCGTCGTGCCAAGGCCGTTCAGCGCTACCTGGTGCTGCAGGGCGTTTCGCCG
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                                                                                                                                                                                                                                                              Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 LeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGln 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 13263)

2 (bases 1 to 13263)

Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Golfry, L., Tolentino, E., Lagrou, M., Garber, R.L., Golfry, T., Tolentino, E., Colfry, T., Colfry, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stover.C.K., Pham,X.O., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T. Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 AAGGGCGGCGATGCTTCCGGTGAAGGTGCCAATGGCGGCGTCGACCCGAACGCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spe Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
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Nature 406 (6799), 959-964 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hancock, R.E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE004530 13263 bp DNA linear BCT 30-AUG-
Pseudomonas aeruginosa PA01, section 91 of 529 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:9946865
                                                                                                                                                                                                                                                                                                                                                                                                                                       Lory, S. and Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCT 30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spencer, D.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4692
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DDVVVNDDGSIDVFTTFADFISVNEALAAAGFKGDEAEVTMIPSTTATLDLETAQKVL
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5590. .6114
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LHVVFRSVREVIRTHGPTALSIBQVFMARNADSALKLGQARGAAIVAAMEEGLSVAEV
TASQVKQAVVGTGGADKQQVQMMVMHLLKLTQKPQIDASDALAIALCHAHTQQSLVPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product "Holliday junction resolvase RuvC"
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TNLEAGDVLFVDEIHRLSPIVEEVLYPAMEDFOLDIMIGEGPAARSIKLDLPPFTLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAQDTSTLVKIPGVGKKTAERLLVELKDREKAWENMPTIAPLVMEPRASATVSSAEAD
AVSALIALGEKPQEASRAVAAVPGEDLSSEEMIRQALKGMV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTLHTHLVVREDAHLLYGFAEKRERELFRELIRLNGVGPKLALALMSGLEVDELVRCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTRAGMLTNPLRDRFGIVQRLEFYNVEDLATÍVSRSAGILGLEIEPQGAAEIAKRAR
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              REFERENCE
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                                                                                                                  KEYWORDS
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                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                    LOCUS
                                                                            ORGANISM
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US-09-674-779B-2 (1-172) x AE004530 (1-13263)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11930 AAGGGCGGCGATGCTTCCGGTGAAGGTGCCAATGGCGGCGTCGACCCGAACGCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11879 AAATTTGCTGCGCTGGCTCTGGCCATGGCTGTG------GCTGTGGGTTGCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12041 CGTGCGATCACCACC------TTCTACTTCGAGTACGACAGCTCCGACCTG 12085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11984 GGCTAT---GGCGCCAACAGCGGTGCCGTTGACGGCAGCCTGAGCGACGAAGCCGCTCTG 12040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12086 AAGCCGGAAGCCATGCGCGCTCTGGACGTACACGCGAAAGACCTG---AAAGGCAGCGGT 12142
                                                                                                                                                                                                                                                                                                      12323 CAGTCCTGGGCTCAGAACCGTCGCGTCGAGCTG 12355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12203 CTGGGCGAGCGTCGTGCCAAGGCCGTTCAGCGCTACCTGGTGCTGCAGGGTGTTTCGCCG 12262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSer 119
                                                                                                                                                                                                                                                                                                                                                                                                                  140 AlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGlu 159
                                                                                                                                                                                                                                                                                                                                           160 GluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 LysproGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 Lys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn
                                                            Salmonella typhimurium LT2.
Salmonella typhimurium LT2
                                                                                                                                                                                           AE008730 20941 bp 1 Salmonella typhimurium LT2, section
                  Salmonella
                                         Bacteria; Proteobacteria;
                                                                                                                               AE008730.1
                                                                                                                                                      AE008730 AE006468
                                                                                                                                                                         genome
                                                                                                                                                                                                                                                                                                                                                                                              GCCCAGCTGGAACTGGTTTCCTATGGTAAAGAGCGTCCGGTCGCTACCGGCCACGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGln 139
(bases 1 to 20941)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mednvvdhtsmwslisnasivvqlvmltlvaasvtswimiforg
namraakkaldafeerfwsgidlsklyrqagsnpdpdsgveqifragfkefsrlkqop
gydpdaymegvaramkvaisreeekleaslpflatvgstspyvglfgtvwgimnsfrg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LATVQQATLATVAPGIAEALIATAIGLFAAIPAVIAYNRFSARSEMLIGRYYTFADEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="tolk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="TolR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="tolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PA0970"
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306.00
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40.94%
35.54%
                                                                                                                               GI:16419241
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Matches:
                                         gamma subdivision; Enterobacteriaceae;
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RBS

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FEATURES
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The analyses of ribosome binding sites and promoter binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          were kindly provided by Heladia Salgado, Julio Collado-Vides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ecocyc.PangeaSystems.com/ecocyc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Pedro Romero and Peter Karp at EcoCyc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, Mo 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W., Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F., Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A., Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W., Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K. Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salmonella typhimurium Genome Sequencing Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 413 (6858), 852-856 (2001) 21534948
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                                   /product="succinate dehydrogenase, /protein_id="AAL19676.1" /db_xref="GI:16419242"
                                                                                                                                                               /note="similar to E. coli succinate dehydrogenase, cytochrome b556 (AAC73815.1); Blastp hit to AAC73815.1 (129 aa), 92% identity in aa 1 - 129"
/translation="MIRNVKKQRPVNLDLQTIRFPITAIASILHRVSGVITFIAVGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="putative -10_signal for sdhc; RegulonDB:STMLTH004697"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative -35_signal for sdhC;
RegulonDB:STMLTH004697"
                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                           /EC_number="1.3.99.1"
/EC_number="1.3.5.1"
                                                                                                                                                                                                                                                                                                                                                          /note="putative RBS for sdhC; RegulonDB:STMS1H001042"
179. .568
                                                                                                                                                                                                                                                                                                                         /gene="sdhC"
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="sdhC"
                                                                                                                                                      codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Salmonella typhimurium LT2"
/strain="LT2; SGSC 1412; ATCC 700720"
/db_xref="ATCC:700720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="STM0732"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="LT2"
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                                                                                        cytochrome b556"
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DLVVDMGQFYAQYEKIKPYLLNNGQNPPAREHLQMPEQREKLDGLYECILCACCSTSC
                                 EKDPSLSFRRSCREGVCGSDGLNMNGKNGLACITPISALTQPGKKIVIRPLPGLPVIR
                                                      /product="succinate dehydrogenase, Fe-S protein"
/protein_id="AAL19679.1"
/db_xref="GI:16419245"
/translation="MMKLEFSIYRYNPDVDNAPRMQDYTLEGEEGRDMMLLDALIQLK
                                                                                                                                                                                                                      /note="similar to E. coli succinate dehydrogenase, sulfur protein (AAC73818.1); Blastp hit to AAC73818.aa), 96% identity in aa 1 - 238"
                                                                                                                                                                                                                                                                                                                    /gene="sdhB"
/EC_number="1.3.99.1"
/EC_number="1.3.5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTFAHVDPVKEPIPVIPTCHYMMGGIPTKVTGOALTVNEOGEDVVIPGLFAVGEIACV
SVHGANRLGGNSLLDLVVFGRAAGLHLQESIAEOGVLRDASESDVEGSLERLNRWNNN
RNGEDPVAIRKALQECMOHNFSVFREGGAMAKGLEQLKVIRERLKNARLDDTSSEFNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="succinate dehydrogenase, flavoprotein subunit"
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/protein_id="AAL19678.1"
/db_xref="Gi:16419244"
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GLPESRLDDGRIYQAPFGGGSKANGGGBQARTAAAADRTHALLHTLYQQNLKNHTTI
TSEWYALDLVKNODGAVVGCTALCIETGEVVYFKARATVLATGGAGRIYQSTNAHI
TGDGVCMALRAGVPVQDMEMQFHPTGIAGAGVLVTEGCGREGGYLLNKHGERFMERY
                                                                                                                                                                                                                                                                                                                                                                                                                     2689.
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/gene="sdhB"
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                                                                                                                                                                                        transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative RBS for sdhB; RegulonDB:STMS1H001045"
2689. .3408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to E. coli succinate dehydrogenase, flavoprotein subunit (AAC73817.1); Blastp hit to AAC73817.1 (58 aa), 97% identity in aa 1 - 588"
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AAC73817.1 (
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/EC_number="1.3.99.1"
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FEAWTGFFSSAFTKVFTLLALFSILIHAWIGMWQVLTDYVKPLAVRLILQLVIVVALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="succinate dehydrogenase, hydrophobic subunit"
/protein_id="AAL19677.1"
/db_xref="GI:16419243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative RBS for sdhA; RegulonDB:STMS1H001044"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYVIYGFVVVWGV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="sdhD"
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892. .897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="sdhA"
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/EC_number="1.3.99.1"
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                                                                                                                                                                                                                                                                                         19634 ATGTCATCTGAAGAGCAAGCGCGTCTGCAGATGCAGCAGCTGCAGCAGAACAACATCGTT 19693
                                                                                                                                       55 -----AsnAspGluThrValLysAlaLeuAlaSerLysLeuPro-----SerLeuVal 70
                                                                                                                                                                                                                                                41
                                           71 TyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGln 90
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                           TyrThrGlyValIleTyrThrGlyValAlaProLeuValAsp------
                                                                                                                                                                                                                                                                                                                                       ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
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DLFDEFAGKHKEHLGTGDVKYHMGFSSDIETBGGLVHLALAFMPSHLEIVSFVVMGSV
RARLDRIDEPSSNKVLFITIHGDAAVTGGGVVGETLMSKARGYEVGGTVRTYINNOV
GFTTSNFLDARSTPYCTDIGKMVQAPIFHVNADDPEAVAFVTRLALDFRNTFKRDVFI
DLVCYRRHGHNEADESGATOPLMYQKIKKHPTPRKIYADKLEADKVATLEDATEMVNL
YRDALDAGECVVKEWRPMNMHSFTWSPYLNHWADEAVRAVEMKRLOELAKRISTYPE
AIEMOSRVAKIYGDGAAMAGEKLFDWGGAENLAYATLVDEGIPVRLSGEDSGRGTFF
RHAVIHNOTNGSTYTPLOHIHSGOGOFKVWDSVLSEEAVLAFEYGYATAEPRTLTIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to E. coli 2-oxoglutarate dehydrogenase (decarboxylase component) (AAC(73820.1); Blastp hit to AAC(73820.1 (933 aa), 94% identity in aa 1 - 933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="putative -10_signal for sucA; RegulonDB:STMLTH004698"
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KGLNPTRAIGHIKSMLLQRSA"
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GHQHANLDPLGLWKQERVADLDPSFHDLTEADFQETFNVGSFASGKETMKLGELLDAL
KQTYCGPIGAEYMHITSTEEKRWIQQRIESGRAAFSADEKKRFLNELTAAEGLERYLG
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/db_xref="GI:16419246"
/translation="MQNSALKAWLDSSYLSGSNQSWIEQLYEDFLTDPDSYDANWRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            component"
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CAEQNMQVCVPSTFAQVYHMLRRQALRGMRRPLVVMSPKSLLRHPLAVSTLDELANGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="2-oxoglutarate dehydrogenase decarboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Walin, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T. G., Sebalhia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feitwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Parry, C., Quail, M., Rutherford, F., Simmonds, M., Skelton, J., Parry, C., Quail, M., Rutherford, B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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AL627268.1 GI:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 294050)
Parkhill,J.
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                                                                                                                                                                                                                                                                                                                                                                                  (URL, http://www.sanger.ac.uk/Projects/S_typhi/)
                                                                                                                                                                                                                                                                                                                                                                                                               on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of S. typhi sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                 /EC_number="5.4.99.9"
/note="Similar to Klebsiella pneumoniae probable
/note="Similar to Klebsiella pneumoniae probable
udp-galactopyranose mutase rfbD SW:GLF1_KLEPN (048485)
udp-galactopyranose mutase SW:GLF_ECOLI
Escherichia coli udp-galactopyranose mutase SW:GLF_ECOLI
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                                                                                                                                                                                                                                                                                         Typhi"
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                                                                                                                                                                                                                                                                                                             /organism="Salmonella enterica subsp. enterica serovar
                                                                                                                                          /gene="STY0759"
                                                                                                                                                                                          /gene="STY0759"
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8.9e-42"
                                                                                                                                                                                                                                                                                                          /db_xref="SUTREMBL:Q8XFZ1"
/db_xref="SUTREMBL:Q8XFZ1"
/translation="MKRLCYFVNSDWYFDLHWTERAIAARDAGYEIHIISHFIGEEII
KKFKTLGFICHWSLVAQSFNNFVFFRAFLNARKIIKEINPDLHCITLKPCLIGGVS
ARRSNSPVVISFVGLGRIFLYNTVPMRILRALTVLVYKYIAQNKRGVFIFEHDKDRRK
ISRLVGIDYHKTIVIEGAGINPDIYKFSIEKKHEIPIVLFASRMLWSKGLGHEAKK
ISRLVGIDYHKTIVIEGAGINPDIYKFSIEKKHEIPIVLFASRMLWSKGLGHEAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     galactosyltransferase wbbo or rfbF TR:Q48487 (EMBL:L31762) (377 aa) fasta scores: E(): 0, 69.1% id in 375 aa, and to Serratia marcescens galactosyltransferase wbbo or rfbF TR:Q54481 (EMBL:L34167) (380 aa) fasta scores: E(): 0, 55.2% id in 375 aa"
                                                                                                                                                                                                                                        YLLKNPQIRLEMGANGRKRVKELFSSILVINKTLQIYKDTIGC"
                                                                                                                       /note="Pfam match to entry PF00534 Glycos_transf_1, Glycosyl transferases group 1, score 152.20, E-value
                                                                                                                                                                                                                                                             ILROKNIHFVLNVAGILAEDDKDAIPLELIHHWHNEGLINWLGRSSNYYELIQKSNIV
ALPSIYPEGVPRLLLEASSVGRACIAYDTGGCDSLIIHNYNGLIVKSNSAQELAVELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="galactosyltransferase"
/protein_id="CAD05183.1"
/db_xref="GI:16501956"
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2332. .3465
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/protein_id="CAD05182.1"
/protein_id="CAD05182.1"
/db_xref="g1:16501955"
/db_xref="g1:16501955"
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%LDTSSYRIFASRVQDTYGRSCRMNLPFIRVPSTVETITYAMRPERFSEVRTQVDD
SLLDTSSYRIFASRVQDTYGRSCRMNLPFIRVPSTVETITYAMRPERFSEVRTQVD
                                                        'gene="STY0762"
                                                                                                                                                                                                 /gene="STY0761"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similar to Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycosyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSARRVTKIMQRKKILIVGAGLSGAVIARQLAEQGHVVNIIDQR SHIGSNAYDARDEHTGIMVYVGGPHIFHTDNETVMNYVKYAEMMPYINKVKATVNGQ VFSLPINLHTINQFFGYACSPDDARKLILQKCDSTILEPQNEEQQALRFIGKELYEAF FKGYTIKQWGLHPSALPASULKRIPVERNYDDNYFNHKFGGIPKFGYTOMKSIVEHE WIAVELCRSFTGEMRINYDHVFFSGALDAFYSCQYGRLEYRTLDFKKIICQSDYQGCA VMNYCSIDTPYTRITEHKYFSFWERHHAASICYQEYSRECEAGDIPYYPVRRADKMDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3/posyl transferases, score 12.60, E-value 0.013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQTVSFVGMIIDRKVLNNHLNDIYDELFLYYDDFFFGYKLVLSGQKIRYSPEIKFIHD
ISIHGRCICPEWKVYYLCRNLLLLRKLLPVPRIFSVLSIVLRLSKYLAILPWQRKKFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLYFIWQGILHGLKGISGKYH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="STY0760"
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/protein_id="CAD05181.1"
/db_xref="GI:16501954"
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                                                                             /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="PS00017 ATP/GTP-binding site motif A (P-loop)" 51/2. .6945
/gene="STY0767"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="STY0765"
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permease protein (pseudogene)"
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/gene="STY0764"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="STY0764"
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/gene="STY0762"
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/note="Similar to Mycobacterium tuberculosis hypothetical 32.3 kDa protein cy13d12.17 rv3783 or mtcy13d12.17 TR:P72049 (EMBL:280343) (280 aa) fasta scores: E(): 1.4e-26, 42.2% id in 187 aa, and to Yersinia enterocolitica O-antigen export system permease protein RfbD rfbD SW:RFBD_YERBN (056902) (259 aa) fasta scores: E(): 9.3e-19, 29.4% id in 187 aa. This CDS contains a stop believed to be correct."
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/gene="STY0762"
/gene="STY0762"
/note="Pfam match to entry PF01061 ABC2_membrane, ABC-2
tune transporter, score 21.40, E-value 5.2e-07"

gene

VEALKKIDFTLTEGNRLALIGHNGSGKTTLLRVLAGAYKPTSGKYECIGRVTSLIDPM MGMDGELTGLENIKLRGLFLGLSKNEIKNITEDVIEFSELGDFIKIPVRTYSSGMVLR LGFSISTAINPEILLMDEWMSVGDSDFKRKAEMRLNSFISKAGIMVMATHDDELAKSV /transl_table=11
/product="putative polysaccharide export ABC transporter
/problem protein"
/protein_id="CAD05185.1"
/db_xref="GI:16501957" /note="Similar to Mycobacterium tuberculosis hypothetical 30.0 kDa protein cy13d12.15 rv3781 or mtcy13d12.15 TR:P72047 (EMBL:280343) (273 aa) fasta scores: E(): 0, 43.8% id in 233 aa, and to Yersinia enterocolitica O-antigen export system ATP-binding protein RfbE rfbE SW:RFBE YEREN (056903) (239 aa) fasta scores: E(): 0, 45.3% id in 225 aa" /db_xref="SPTREMBL:Q828D5" /translation="MKISCKNVGVILPIFNSSHRSPKKTFLQAASGGRIGSSNTGIIE

/note="Similar to Mycobacterium tuberculosis hypothetical 71.5 kDa protein rv3808c or mtv026.13C TR:053585 (EMBL:AL022076) (637 aa) fasta scores: E(): 0.00015, 26.6% id in 467 aa, and to Mycobacterium tuberculosis hypothetical 33.9 kDa protein cy13d12.16 rv3782 or mtcy13d12.16 TR:P72048 (EMBL:280343) (304 aa) fasta scores: E(): 0.16, 25.6% id in 215 aa, and to Klebsiella pneumoniae RfbE rfbE TR:048482 (EMBL:141518) (297 aa) fasta scores: E(): 0.3, 23.6% id in 233 aa. This CDS contains at least one stop codon and frameshift. The sequence has been checked and is believed to be correct /product="conserved hypothetical protein (pseudogene)"

gene

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Query Match:
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu 150
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                                                                                cydB gene; cytochrome d terminal oxidase; pal gene; peptidoglycan-associated lipoprotein; tolA gene; TolA protein; tolB gene; TolB protein; tolQ gene; TolQ protein; tolR gene; TolR protein; ybgC gene; YbgC protein; ybgE gene; YbgE protein; YbgF; ybgF gene; ybgT gene; ybgT protein.
                                                                                                                                                                                                                                          ECH297885 6967 bp DNA linear BCT 12-OCT-2001 Erwinia chrysanthemi cydB gene (partial), ybgT gene, ybgE gene, ybgC gene, tolQ gene, tolR gene, tolA gene, tolB gene, pal gene and
                                                      Erwinia chrysanthemi
                                                                                                                                                                                        AJ297885.1 GI:16116629
                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                    Erwinia chrysanthemi.
                  Pectobacterium
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(bases 1 to 6967)
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protein yveR TR:P71057 (EMBL:271928) (344 aa) fasta
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/gene="STY0767"
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Indels:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ray,M.C., Vianney,A., Cotte-pattat,N. and Lazzaroni,J. characterization of the Erwinia chrysanthemi tol-pal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Villeurbanne cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 6967)
Lazzaroni, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=2
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                                                                                                                       /gene="tolQ"
1326 .2012
/gene="tolQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Erwinia chrysanthemi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMFGRITKEHVEQNSHSLY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="3937"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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925. .1329
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                                                                                                         /function="outer membrane integrity"
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mat_peptide
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GISQVTDGRSNNTEPTWFPDSQTLAYTSDQAGRPQIKKIGINGGAPQRLTWEGSGNQD
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                                                                                                                                                                                                                                                                                                                 SEISSDGKFLVMVSSNSGAQHIAKQDLVTGGVQVLTDTFLDETPSIAPNGTMVIYSSK
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                                    /gene="pal
                                                                   /gene="pal"
5234. .5740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGRTCTLRIRLAPDGLLVDVKSEGGDPALCQAAIAAAKQARIPKPPSSDVYEAFKQRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="inner membrane protein interacting with TolQ and
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2025. .2450
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CDS gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
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5516 TCCTACAAAGTGACTGTTGAAGGTCACGCGGACGAACGCGGTACGCCGGAATACAACATC 5575
                                                                               5456 ATTCGCCCTGACTTCGCTCAGATGCTGGATGCGCACGCTGCTTTCCTGCGCAGCAACCCG 5515
                                                                                                                                                            5396 CTGCAGATGCAGGAACTGCAGCGCAACAATATCGTTTACTTCGATCTGGACAAATACGAC 5455
                                                                                                                                                                                                                                                                                                                        5306 ------AACAAACACGCTAATAACGACCAGTCTTCCCTGAACGGCGGCGCTGGC 5353
                                                                                                                                                                                                                                                                                                                                                                                                       5261 CTGATGTTGGCTCTGCCGGTGCTGGCTGTTGCCGCATGTAGCTCC----- 5305
                                                                                                                                                                                                                                                        5354 ATGGAAAAT----
                         79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                  61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                              21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetMetLeuHisīleGlnīleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                                                                 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
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5297
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5825. .6571
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5750 .6574
/gene="ybgf"
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1740 c 1992 g 15
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SQSGGQSSSAASSAAGAGNAVTSAPAASSDTGAANSANADSAAAPAMTGDANTDYNTA
ASLVLEKKQYDQAIVAFQNFVKKYPDSTYQPNANYNLGQLFYNKGKKDDAAYYFANYV
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287.50
55.17%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5576 GCGCTGGGCGAACGTCGTGCCAACGCTGTGCAGATGTACCTGCAGGGCAAAGGCGTGTCT 5635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5696 GAAGCTGCATGGTCCAAAAACCGTCGTGCCGTTCTGGTATAC 5737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Risen, J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M.B., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 10029)
2 (bases 1 to 10029)
Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J., Nierman, W.C., Feldblyum, T.V., Ohta, N., Maddook, J.R., Potocka, I., Heidelberg, J.F., Alley, M.R.K., Ohta, N.D., Ely, B., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Berry, K., Witterback, T., Tran, K., Wolf, A., Vamathevan, J., Bernolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and Trans, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caulobacter crescentus CB15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (31-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of Caulobacter crescentus Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
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                                                                                                    VLRPLLTLTRAEIRDALTREGETWLDDPANLDLRYARARARAGALTPLLPVRESPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(79. .1305)
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RSRATTRITTDPAIDTSPSFSPDGTKIVFNSDRGGQAQIYVMNTDGSGVRRISYGGGR
YTTPVWSPRGDFIAFTKQTGGEFHIGVMRADGGDERLLTTSYLDEGPTWAPNGRVLMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPGTSSPDPVVKAASDRAIRALFAASPFAYLPSDLYGQKIALNFNAKQACSR*
/note="similar to PID:1103861 SP:P50599; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="identified by Glimmer2; putative"
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Percent Similarity:
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                                                                                                                                                                                                    {	t RVAGRLLR} {	t RVRDFATADGADRIDRKAAAMALARLEVDESGLDSLDRRYLRAMIENYGG}
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EANDYLFIDEIHRLSSNVEEILYPAMEDHVLDLVIGEGPSARSIRIDLAPFTLVAATT
RAGMLATPLRDRFGIPIRLEFTTPAELRHVLOHAARKMGAPLTDDGADEIAKRARGTP
                                                                                                                                                                                                                                                                                                    /product-"Holliday junction DNA helicase RuvB" /protein_id="AAK25198.1" /db_xref="GI:13424920" /taanslation="WTRVISGEPQHGDLAPADRALRPQTLAEFVGQEQAKGNLRVFIE
                                                                                                                                         complement(8808. .9425)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transiation="MKASSMRLIRLLTAGLAAVGLAVSLAAISAAGAPRNALIVQALAAGLAYGLALLVGWFWRRARWRLWVLMAACGLALVLTLMNGVSLEGAKRWVALGPVQLHTASIVLFFAAFARGFGDRRVAPIAALIALLLLLYQHDAASSLAWALALAAAALVERPRQAIPWACVAIAGLLAYGAWVEPDTLPAVPYVEGLLDQTFAANPVLGVLAGVLMISLPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="identified by match to TIGR protein family HMM
TIGRO0635"
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LGDSVDQDPPAP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
/protein_id="AAK25197.1"
/db_xref="GI:13424919"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CC3236"
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complement(6915. .7781)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
/protein_id="AAK25196.1"
/db_xxef="GI:13424918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6915. .7781)
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MSETQAGEL LARIDRILDTQIARETTKVEBGLGSLAIVATASPE IGLEGTVWGIMHAF
QNIALSKNTSLAVVAPSIAEALFATAIGLIAAIPAYIAYNKFSTDAGKYAGRLEGFAD
DLSTAIQRRLAERV"
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58.24%
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/protein_id="AAK25195.1"
/db_xref="GI:13424917"
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IfmISAPLLTAGVPLELPKTEAAALQNQDEPITVSIRKDGQIFVGETEIPFENLAPRI
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Conservative:
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                                                                                                                                                          JOURNAL
                                                                                                                                                                                 TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 IleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2698 CCGAAGCCCCAGCCCGTCACGCCGCCGCCCGCTCAGCCGCAGCCGACCCAACCGACGCCT
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA UNGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France,
                                                                                                                                                                                                                                                                                     Salanoubat, M., Genin, S., Artiguenave, F., Gouzy, J., Mangenot, S., Arlat, M., Billault, A., Brottier, P., Camus, J.C., Cattolico, L., Chandler, M., Choisne, N., Claudel-Renard, C., Cunnac, S., Demange, N., Gaspin, C., Lavie, M., Moisan, A., Robert, C., Saurin, W., Schiex, T., Siguier, P., Thebault, P., Whalen, M., Wincker, P., Levy, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                  Boucher, C.A
                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                  Weissenbach, J. and Boucher, C.A. Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ralstonia solanacearum
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 AspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThr 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 GluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia solanacearum GMI1000 chromosome, complete sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://sequence.toulouse.inra.fr/R.solanacearum.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Christian.Boucher@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet Tolosan Cedex. Laboratoire de Genetique Cellulaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INRA, BP27, F31326 Castanet-Tolosan Cedex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="RS04909"
59. .757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="HYPOTHETICAL TRANSMEMBRANE PROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="miscellaneous; hypothetical/global homology"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Ralstonia solanacearum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structures"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVGWWMGRRSLRQA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="structural elements; cell exterior; surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="RSc0557; RS04908"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="pilAl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSRVVEGLALAGQAKALVVENAANAQSSLSLGSASLPASKNVSALNIDSSTGEIAVVY
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                                                                                                                                                                                                                                                                                                /function="structural elements; cell exterior; surface
structures"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATLPPKYAPSECR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYAPAECR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"RS00560; RS04905"
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/function-"small molecule metabolism; biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4289. .4765)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cofactors, carriers; molybdopterin'
/note="Product confidence : probabl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALAFQGKTDEALTQVRRLHNQYWIDYAGDSKLLTLVCTKKLEGLATFCARLKAENLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="PROBABLE MOLYBDENUM COFACTOR BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                 predicted by Homology predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                     Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                        /function="miscellaneous; hypothetical/global homology"
/note="Product confidence : hypothetical
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                                                                                                                                                                                               /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                 codon_start=1/
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US-09-674-779B-2 (1-172) x AL646060 (1-212050)
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182482 GCACAGAACCGCCGCTCCGATATCGTCTAC 182511
                                                                                                                                                                                         182362 AAGCGTGCCGAGGCCGTGCGCCGCGCGCTGTCCTCGCTGGGCGTGCCCGACAGCCAGATG 182421
                                                                                                                                                                                                                                                                                              182302 CTGATCCAGGGCAACACCGACGAGCGCGCGCACCAGCGAGTACAACCTGGGCGCTGGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                          182242 TACCAGGGCCTGCTGACCCAGCATGCGCGCTACCTGCAGTCGCACAACCAGCGCAAGGTG 182301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182182 AGCCCGCTGGCCAAGCGCAGCGTGTACTTCGATTTCGACAGCTACACCGTCAAGCCGGAA 182241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182122 GCCGACACCCGCAACGTGACGCCCGTCGACGTGAGCCGCGATGAACTGACCGGATCCGAAC 182181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182077 CTGGATGACACCTCGAAG-------AACGCCACGGGTGGTGCCGCCGCCGGT 182121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182017 ATCAAGCTGGCGGCGATTGCCGCGCTGCTGGCGCTTGGGCGCTTGCAGCTCGGGTGTGAAG 182076
                                               163 SerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                       143 GluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrp 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 ValileTyrThrGlyValAlaProLeu---ValAspAsnAspGluThrValLysAlaLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAla 24
                                                                                          GAATCCGTGAGCCTGGGCAAGGAAAAGCCGCAGGCCTCGGGCCACGACGAGGAGTCGTGG 182481
                                                                                                                                                                                                                                         ArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerVal 142
                                                                                                                                                                                                                                                                                                                        LeuvalAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGlu 122
                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly---TyrThrGly 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Product confidence : hypothe
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted by Codon_usage predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="RS04903"
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286.50
59.41%
38.24%
33.28%
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                                       196 GCATGTTCTTCCAACAAGAACGCCAGCAATGACGGCAGCGAAGGCATGCTGGGTGCCGGC
                                                                                                              136 ATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCAATTGCG 195
41 TyrThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                        21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                 1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen,R. and Henning,U. Nucleotide sequence of the gene for the peptidoglycan-associated lipoprotein of Escherichia coli K12 Eur. J. Blochem. 163 (1), 73-77 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Data kindly reviewed (19-OCT-1987) by HENNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lipoprotein; pal gene; peptidoglycan-associated lipoprotein. Escherichia coli. Escherichia coli
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698. .711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="pot. stem-loop structure; pot. transcription
terminator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SWISS-PROT:P07176"
/translation="MOLNKVLKGLMIALPYMAIAACSSNKNASNDGSEGMLGAGTGMD
/TGGNGLMSSEGMARLOMQQLQONNIVYFDLDKTDIRSDFAQMLDAHANFLRSNFSYK
VTVEGHADERGTPEYNISLGERRANAVKMYLQGKGVSADQISIVSYGKEKPAVLGHDE
AAYSKNRRAVLVY"
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/protein_id="CAA28771.1"
/db_xref="GI:42257"
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/strain="K12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 GAAGCGGCATACTCCAAAAACCGTCGTGCGGTACTGGTTTAC 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              excC gene; PAL gene; peptidoglycan-associated lipoprotein Escherichia coli.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-JUN-1992) J. Lazzaroni, Lab de Microbiologie et Genetique Moleculaire, UMR 106, CNRS, Bat 405, University Claude Bernard Lyon I, F-69622 Villeurbanne Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1531)
Lazzaroni, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lazzaroni,J.C. and Portalier,R.

The excC gene of Escherichia coli K-12 required for cell envelope integrity encodes the peptidoglycan-associated lipoprotein (PAL) mol. Microbiol. 6 (6), 735-742 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      revised by [3]
3 (bases 1 to 1531)
Lazzaroni, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli excC gene for peptidoglycan-associated lipoprotein.
                           /translation="GQVKFPAWSPYL"
                                                                           /transl_table=11
/protein_id="CAA46672.1"
/db_xref="GI:41359"
/db_xref="SWISS-PROT:P19935"
                                                                                                                                                                                                                                                                                                                                                                                                                                     (29-JUN-1992)
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/gene="tolB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
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                                                                                                                                                                                                                                                                                                                                                       GCAGACCAGATCTCCATCGTTTCTTACGGTAAAGAAAACCTGCAGTACTGGGTCATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                       GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
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AL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Project and NCHGR). The entire sequence was independently determined by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently frames were determined using Genemark Software, kindly supplied by 3032 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Correlating it with other data. Comments to the authors are ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically undated; this is verein MSA No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels while the court of the court o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            names
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            labels. This should allow them to be searched for in Entrez as gene
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Plunkett, G. III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                /function="orf; Unknown"
                                                                                                                                                                                                              /gene="ybgE"
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                                                                               'gene="ybgE"
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                                                                                                                                                                                                                                                                                    /note="factor Sigma70; predicted +1 start at 773447"
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/gene="tolA"
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/note="b0739"
2127. .3392
                                                                                                  PKTVFLIGGAKDVPYDEIIKALNLLHSAGVKSVGLMTQPI"
                                                                                                                    translation-"marargrgrrdikseinivplidvllvllifmatapiiiosve"/translation-"marargrgrrdikseinivplldvllvlllifmatapiiiosve"/translation-"marargrgrrdikseinivplldvllvlllifmatapiiiosve
                                                                                                                                                                           /product="putative inner membrane protein, involved in the tonB-independent uptake of group A colicins" /protein_id="AAC/79832.1" /db_xref="GI:1786959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC73831.1"
/db_xref="GI:178958"
/db_xref="GI:178958"
/translation="mymniddfikasllvklimliligesiaswaiiiqrtrilna
AAREAEAFEDKEWSGIELSRLYQESQGKRDNLTGSSEQIFYSGFKEFVRLHRANSHAPE
AVVEGASRAMRISMNRELENLETHIPFLGTVGSISPYIGLEGTVWGIMHAFIALGAVK
                                                       'gene="tolA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QATLQMVAPGIAEALIATAIGLFAAIPAVMAYNRLNQRVNKLELNYDNFMEEFTAILH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="inner membrane protein, membrane-spanning, maintains integrity of cell envelope; tolerance to
                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                              /function="putative transport; Not classified" /note="0142; 100 pct identical to TOLK_ECOLI SW: p05829"
                                                                                                                                                                                                                                                                                                                                                                                                           /gene="tolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="tolR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="orf, hypothetical protein"
/protein_id="AAC73830.1"
/db_xref="GI:1786957"
                                                                                                                                                                                                                                                                                                     transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="b0738"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="membrane; Colicin-related functions"
/note="0230; 100 pct_identical to TOLQ_ECOLI SW
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/gene="tolQ"
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LLNEAEVLVVCVDPLKMKPRALPKSIVAEFKQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="factor Sigma70; predicted +1 start at 774366"
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/protein_id="AAC73829.1"
/db_xref="GI:1786956"
/translation="MSKIIATLYAVMDKRPLRALSFVMALILAGCMFWDPSRFAAKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNTTLFRWPVRVYYEDTDAGGVVYHASYVAFYERARTEMLRHHH
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/function="orf;
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/note="b0736"
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Best Local Similarity:
Query Match:
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                                                         4972 ---ACTGGTATGGATGCGAACGGCGGCAACGGCAACATGTCTTCCGAAGAGCAGGCTCGT 5028
                                                                                                                                          4912 GCATGTTCTTCCAACAAGAACGCCAGCAATGACGGCAGCGAAGGCATGCTGGGTGCCGGC 4971
                                                                                                                                                                                                                          4852 ATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCAATTGCG 4911
                                                                                              41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                {\tt 21~ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly~40}
                   61
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                                                                                                                                                                                                                                                                    MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
             AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
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gggssidaymydsgavveqykrmqsqessakrsdeqrkmkeqqaaeelrekqaaeqer
lkqlekerlaaqeqkkqaeeaakqaelkqkqabeaakkaaadakakabadakaaeeaa
kkaaadakkkaeaaakaaaeaqkkaebaaaalkkkaeaaaaaaaarkkaatbaaek
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/protein_id="AAC73833.1"
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3525. .4817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="membrane; Colicin-related functions"
/note="0421; 100 pct identical to TOLA_ECOLI SW: P19934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGQIRQVTDGRSNNTEDTWFPDSQNLAFTSDQAGRPQVYKVNINGGAPQRITWEGSQN
QDADVSSDGKFMVMVSSNGGQQHIAKQDLATGGVQVLSSTFLDETPSLAFNGTMVIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="periplasmic protein involved in the tonb-independent uptake of group A colicins" /protein_id="AAC73834.1" /db_xref="GI:1786961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAKLAKIPKPPSQAVYEVFKNAPLDFKP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="factor; Colicin-related functions"
/note="0430; 99.8 pct identical to TOLB_ECOLI SW:
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/gene="tolB"
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JOURNAL
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.

Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7

Nature 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli 0157:H7 of 155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli 0157:H7 EDL933
Escherichia coli 0157:H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE005252.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE005252 AE005174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE005252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCCTGGGTGAACGTCGTGCGAACGCCGTTAAGATGTACCTGCAGGGTAAAGGCGTTTCT 5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThralaargValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 11670)
                                                                                                                                                  complement(93. .260)
                                                                                                                                                                                                                   complement(93. .260)
                                                                                                                                                                                                                                             /note="O-island #35; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                                                                                                        /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:155864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Escherichia coli 0157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
/transl_table=11
                                                                                                                                                                                      /gene="Z0896"
                                                                                                                                                                                                                                                                                                                                                                                                         /serotype="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="EDL933"
                                                          /function="orf; Unknown function"
/note="No significant matches"
                                                                                                                        /gene="20896"
                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:12513661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11670 bp
H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA linear BCT 21-MAR-2001 genome, contig 1 of 3, section 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5328
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                           RSFAIAASFGMAAVLSVIVLGDESGYEMGDVOKTKLAAIEAEWETQPAPAAFTLFGIP
DQEEETNKFAIQIPYALGIIATRSVDTPVIGLKELMVQHEERIRNGMKAYSLLEQLRS
GSTDQAYRDQFWSMKKDLGYGLLLKRYTFNVADATEAQIQQATKDSIPRVAPLKFAFR
IMVACGFLLLAIIALSFWSVIRNRIGEKKWLLRAALKGIPLFWIAVEAGWFVAEYGRQ
PWAIGEVLPTAVANSSLTAGDLIFSMVLICGLYTLFLVAELFLMFKFARLGPSSLKTG
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/db_xref="Gr:12513666"
/txanslation="MMLDIVELSRLQFALTAMYHFLEVPLTLGMAFILLAIMETVYVLS
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MAFFLESTFVGLFFFGWDRLGKVQHMCVTWLVALGSNLSALWILVANGWMQNPIASDF
NFETTMRMEMVSFSELVLNPVAQVKFVHTVASGYVTGAMFILGISAWYMLKGRDFAFAK
/gene="cydB"
/note="z0901" .
                                                                        RYHFEQSSTTTQPAR"
                                                                                                                                                                                                                                                                                                                                                                                  /product="cytochrome d terminal oxidase, polypeptide subunit I" \Gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                        transport"
/note="Residues 1 to 523 of 523 are 100.00 pct identical to residues 1 to 523 of 523 from Escherichia coli K-12 Strain MG1655; B0733"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="enzyme; Energy metabolism, carbon: Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="cydA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Trans1_table=11
/protein_id="AAG55068.1"
/db_xref="GI:12513665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIECFVFERDIPSQYRFFKMFTNLALVIDQLTEANKIL"
complement(2077. .2118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDPHRIVVGIOTLYTTORETFTSESOOLIESALOTLHVMNLNNLETNRDEESHYLAFE
YNVDTSDRITYSAXNEEKKPGCYGOCLVIQDDETDLFNLIKIKIFEARHNYVAOLMSDP
EFMEKESYSAQONRLEPHLLVPAYFPLKTNEPVTQEDYLLLKREFKMNDDFNKLTSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="cydA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSTDRKPVMLLFH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Z0899"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YMSILTPLMKCERSVHDNNRYVTGKDTLLLDYPPSGNQIHFHVFPDESATLVLYFSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="20900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="orf; Unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Z0899"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MSPDNIGSAVNRFSGWPSNDSLKTDKESMTSPVTVQVIKMIAAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAG55067.1"
/db_xref="GI:12513664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(958. .1902)
/gene="Z0898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(958. .1902)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIFSILSSLIDSAISKFQHQIPVNGSVNRELLYEDYTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="orf; Unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Z0898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {	t LSRCLASIHPTLAKNIYETENLSDQKLLHIDCRSTNEIKINIFFGQQREGLIEINSDT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAG55066.1"
/db_xref="G1:12513663"
/translation="MIPSQISENTLEVNATYASETTYDTQKFSDILYSAGCSLKDMAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(454. .876)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="No significant matches"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function="orf; Unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="20897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAG55065.1"
/db_xref="GI:12513662"
                                                   .5431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (2077. .2118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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QATLQMVAPGIAEALIATAIGLFAAIPAVMAYNRLNQRVNKLELNYDNFMEEFTAILH
                       AVVEGASRAMRISMNRELENLETHIPFLGTVGSISPYIGLFGTVWGIMHAFIALGAVK
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AAREAEAFEDKFWSGIELSRLYQESQCKRDNLIGSEQIFYSGFKEFYRLHRANSHAPE
                                                                                                                                                                                                                                                                                                                 /_uuction="membrane; Colicin-related functions" /note="Residues 1 to 230 of 230 are 100.00 pct identical to residues 1 to 230 of 230 from Escherichia coli K-12 Strain MG155: B0737"
                                                                                                                          /protein_id="AAG55073.1"
/db_xref="GI:12513670"
                                                                                                                                                                                                           maintains integrity of
                                                                                                                                                                                                                                                                                                                                                                                                                                        6403. .7095
/gene="tolo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ybgC"
/function="orf; Unknown function"
/note-Tresidues 1 to 134 of 134 are 100.00 pct identical
to residues 1 to 134 of 134 from Escherichia coli K-12
Strain MG1655: B0736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MNTTLFRWPVRVYYEDTDAGGVVYHASYVAFYERARTEMLRHH
FSQQALMAERVAFVVRKMTVEYYAPARLDDMLEIQTEITSMRGTSLVFTQRIVNAENT
LLNEAEVLVVCVDPLKMKPRALPKSIVAEFKQ"
                                                                                                                                                                                                                                /product="inner membrane protein,
                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Z0905"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="tolQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="orf, hypothetical protein"
/protein_id="AAG55072.1"
/db_xref="GI:12513669"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEIWHGLLLMWAVCAGVIHGVGFRPQKVLWQGIFCPLLADIVLIVGLIFFFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MIDTEVLRFIWMLLVGVLLIGFAVTDGFDMGVGMLTRFLGRNDT ERRIMINSIAFHDGNOVMLITAGGALFAAWPMVYAAAFSGFYVAMILVLASLFFRPV GEDYRSKIEETRWRNMDWGIFIGSFVDLVIGVAFGRLLQGVPENVDEXFLLYTGN FFQLLNFFGLLAGVVSVGMITTQGATYLQMRTVGELHLRTRATAQVAALYLLLYTGLAGVWLMGIDGYVSVGMITTQGATYLQMRTVGELHLRTRATAQVAALYLLVFALAGVWLMGIDGYVKSTMDHYAASNPLNKEVVREAGAWLVNFNNTPILMAIPALGVVLBLGVVLTAGLILTITAGTAMDKAAWAFVFSSLTLACIIITAGTAMFPFWMPSSTMMNASLTMMDATSSQLTLILTITAGTAMDKAAWAFVFSSLTLACIIITAGTAMFNASSGMIVMDATSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6002. .6406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSKIIATLYAVMDKRPLRALSFVMALLLAGCMFWDPSRFAAKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="orf, hypothetical protein"
/protein_id="AAG55071.1"
/db_xref="GI:12513668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MG1655: B0735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="orf; Unknown function"
/note="Residues 1 to 97 of 97 are 100.00 pct identical to residues 1 to 97 of 97 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLNVMTWVAVVLVPIILLYTAWCYWKMFGRITKEDIERNTHSLY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Z0904"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ybgE"
/note="Z0903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="cytochrome d terminal oxidase polypeptide subunit II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ybgE"
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/db_xref="GI:12513667"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note* Residues 1 to 379 of 379 are 100.00 pct identical to residues 1 to 379 of 379 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="enzyme; Energy metabolism, carbon: Electron
transport"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="cydB"
                                                                                                                                                                                                                                                                                                     _start=]
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                                                                                                                                                                                                              cell
                                                                                                                                                                                               envelope; tolerance to group A
                                                                                                                                                                                                                                membrane-spanning,
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 ThralaargValLeuValAlaGlyHisThraspGluArgGlySerArgGluTyrAsnMet 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
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             Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K., Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
                                                                                                                                                                                                                                                Complete and shotgun sequencing; hrsa; ybgB; cydA; cydl; cyd2; ybgE; ybgC; tolQ; fii; tolR; tolA; cim; excC; lky; ybgF; nadA; nicA; pnuC.
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D90713.1 GI:1651326
                                                                                                                                                                                                       Escherichia coli(strain:K12) DNA, clone:Kohara clone #178.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                     Escherichia coli genomic DNA.
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718-kb DNA sequence of the Escherichia coli K-12 genome
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Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Salto, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yanamoto, Y., and Yano, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Technology, Res. & Edu. Center for Genetic Info.; Takayama, Ikoma, Nara 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The systematic sequencing of the Escherichia coli genome in Japan Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Members: (1995.4 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Address: National Institute of Basic Biology, Okazaki, 444, Japan E-mail: kishori@nibb.ac.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Nucleotide position 767359-783777 from the initiation site of ThrA (0 min.).~This clone is from Kohara_lambda miniset library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="K12"
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                                                                                                                                                                                                                                               transl_table=11/
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                                                                                                                                                                                                                                                                                         /product="Cytochrome d ubiquinol oxidase subunit II (EC
                                                                                                                                                                                                                                                                                                                                                                         similar to SwissProt Accession Number P11027"
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similar to SwissProt Accession Number P11026"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAA35399.1"
/db_xref="GI:1651327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLSLLSYTGTPTAAGVAQQARAWLTPVQCYNKIPWDVKKLNKAGENVPESYSLLKMPP
VGCLISALKKAEDRQEVILRLENPAESATCDATVAFSREVISCSETMMDEHITTEENQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGHDOMPLOONIFEVMDKLREIYPORKFYMSRFEEVFEKIEAORDNLATLKGEFIDGK
YMRVHRTIGSTRMDIKIAHARIENKIVNLLEPLATLAWTLGFEYHHGLLEKMWKEILK
NHAHDSIGCCCSDKVHREIVARRELAEDMADNLIRFYMKKIADNNPOSDADKLVLFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Cytochrome d ubiquinol oxidase subunit I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSNLSGPFLPGQSRTFSYRLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEFLWQSSDGSEVTAQVLPLGYAIGKYLPADENGLRKRLDSYFDVLEKASVTKEILLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEYKYYVLDGQTAILEDYFAVKPENKDRVKKQVEAGKLIIGBWYTQTDTTIVSAESIV
RNLMYGMRDCLAFGEPMKIGYLPDSFGMSGQLPHIYNGFGITRTMFWRGCSERHGTDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to SwissProt Accession Number P54746"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="cyd1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="cyd1"
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/protein_id="BAA35398.1"
/db_xref="GI:4062319"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLGLAGITEGAIPMAIEDPLRVIGSFVLGSMVTGAIVGAMNIGLSTPGAGIFSLFLLH
DNGAGGVMAAIGWFGAALVGAAISTAILLMWRRHAVKHGNYLTDGVMP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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12614 TCCCTGGTGAACGTCGTGCGAACGCCGTTAAGATGTACCTGCAGGGTAAAGGCGTTTCT 12673
                                                                                                                                                                                            12494 ATCCGTTCTGACTTCGCTCAAATGCTGGATGCACATGCAAACTTCCTGCGTAGCAACCCG 1255:
                                                                                                                                                                                                                                                                                           12434 CTGCAAATGCAACAGCTGCAGCAGAACAACATCGTTTACTTCGATCTGGACAAGTACGAT 12493
                                                                                                                                                                                                                                                                                                                                                                                             12377 ---ACTGGTATGGATGCGAACGGCGAACGGCAACATGTCTTCCGAAGAGCAGGCTCGT 12433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12317 GCATGTTCTTCCAACAAGAACGCCAGCAATGACGGCAGCGAAGGCATGCTGGGTGCCGGC 12376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12257 ATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCAATTGCG 12316
                                                                                                                                                                                                                                79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                                                                                                                          61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                         41 TyrThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                              SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                               TCTTACAAAGTCACCGTAGAAGGTCACGCGGACGAACGTGGTACTCCGGAATACAACATC 12613
                                                                                                                           ThralaargValLeuValAlaGlyHisThraspGluargGlySerargGluTyrasnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="tolQ"
8343. .9035
/gene="fii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF_ID:o178#6 similar to PIR Accession Number B25980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mnttlfrwpvrvyyeDtDAGGvvyHASyvAFyeRARTEMLRHHHFSQQALMAERVAFVVRKMTVEYYAFARLDDMLEIQTEITSMRGTSLVFTQRIVNAENTLLNEAEVLVVCVDPLKMKPRALPKSIVAEFKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="15.5k protein (tolAB operon 5' region)."
/protein_id="BAA35402.1"
/db_xref="GI:4062321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to PIR Accession Number A25980"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ybgC"
/note="ORF_ID:o178#5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELEIWHGLLLMWAVCAGVIHGVGFRPQKVLWQGIFCPLLADIVLIVGLIFFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="fii"
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/db_xref="GI:4062320"
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33.16%
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Escherichia coli O157:H7 DNA, co
AP002553 BA000007
AP002553.1 GI:13360271
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Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
                                                                                                                                                                                                                                                                                                                                                                                             Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Ishii,K., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and Shinagawa,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comparative analysis of the whole set of rRNA operons between an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohnishi, M., Murata, T., Nakayama, K., Kuhara, S., Hattori, M., Kurokawa, K., Yasunaga, T., Yokoyama, K., Makino, K., Shinagawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shiga toxin 1 genes of the enterohemorrhagic Es 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S., Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., 1
                                                                                                                                                                                                                                                                                                                              0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinagawa, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto, K., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi,T
                                                                                                                Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:ken@gen-info.osaka-u.ac.jp, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
                                                                                                                                                                                                                                                      5 (bases 1 to 297816)
Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGCGGCATACTCCAAAAACCGTCGTGCGGTACTGGTTTAC 12775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                        Submitted (26-JUN-2000) Ken Kurokawa, Osaka University,
                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20564182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet. Syst. 74 (5), 227-239 (1999)
                                                                                              .-6-6879-2047)
                                                                     project
                                            Location/Qualifiers
/organism="Escherichia coli 0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Sakai outbreak
                        .297816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome, section 4/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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DGNALFRQDLAEMTNOSQCEDPEAGAQAAQWELMYVALDGNIGGMYNGGGLAMGTMDIV
KLHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
KLHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
KJHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
KJHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
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KJHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
KJHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
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KJHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ECs0755"
2781. .3686
/gene="ECs0755"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ECs0754"
1245. .2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_strain="RIMD 0509952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:83334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to SUCD_ECOLI gi|1786949 percent identity
100 in 289 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ECs0753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-probable transcriptional regulator, similar to transcriptional regulators e.g. glycine cleavage system transcription activator (gcv operon activator) - Escherichia coli gi|411043|sp|P32064|GCVA_ECOLI percent identity 31 in 300 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LADIGEALKTVLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAYIKEHVTKPVVGYIAGVTAPKGKRMGHAGAIIAGGKGTADEKFAALEAAGVKTVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDMLTYKVKLDEAGVENIGPNCPGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYE
AVKQTTDYGFGQSTCVGIGGDPIPGSNFIDILENFEKDPQTEAIVMIGEIGGSAEEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mSILIDKNTKVICQGFTGSQGTFHSEQAIAYGTKMVGGVTPGKG
GTTHLGLPVENTVREAVAATGATASVIYVPAPFCKDSILEAIDAGIKLIITITEGIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="succinyl-CoA synthetase alpha subunit"
/protein_id="BAB34177.1"
/db_xref="GI:13360213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ECs0754"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ECs0753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEFLRTPLESHSKKRIFLNDTGKYYLGIVKETLNKLERDTNTIMTWQPTVQVIELAVN
PTFSTHWLIPNLHEFTKLHPDIIVNIHSLANNGDFLNREYDAVIMRENFCAPWAEVEY
LFEEEILPVCSGSLLAMSDQKLSVAELLTELPLLHQSTRITGWEEWFALSGVSSPLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=1
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                                                                                                                                                                           /note="probable cob(I)alamin adenosyltransferase, similar to cob(I)alamin adenosyltransferases (corrinoid adenosyltransferases) e.g. [Escherichia coli]
                                                                                                                                                                                                                                                                                   complement(3720. .4322)
/gene="ECs0756"
                                                                                                                                                                                                                                                                                                                                                                                                                             NGPREDLLSMLIAAVRSNLGVALLPREAIQHDLDSGDMVIPCDVPIRTGNREIMTWOE
EKSDSPHLQQEREWLLAKSVVPQEM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative transcription regulator"
/protein_id="BAB34178.1"
/db_xref="GI:13360214"
                                                                                                                                         gi|115148|sp|P13040|BTUR_ECOLI percent identity
                                                                                                                                                                                                                                                                                                                                                                                                   complement(3720. .4322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                          /gene="ECs0756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MRGKIPKTELLVTFEVVARHESYTRAAEELALTQSAVFRQVSAL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/transl_table=11
                                     /evidence=not_experimental
                                                                      /codon_start=l
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Query Match:
DB:
                                       Percent Similarity:
Best Local Similari
                                                                                                                          Alignment Scores:
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                                   Similarity:
                                                                                                                                                                                                                                                                                                /gene="ECs0759"
                                                                                                                                                                                                                                                                                                                                                                                              FLGCSLTAIGEKGSAIVHALDSLAHAMLKLTGYVMLFAPLTVFAAISALIAERGLAVM
VSAGIFMGEFYFTMLLLWVLLIGLAIVYVGPCIRRLTBALSEPALLAETTSSSEAAFP
GTLEKLEQFGYSPKLASFVLPIGYSFNLVGSMAYCSFATVFIAQACNIHLSIGEQITM
LLILMLTSKGMAGVPRASMVVIAATLNQFNIPEAGLILLMGVDPFLDMGRSATNVMSN
                                                                                                                                                                                                                                                                                                                                                                complement(7533. .7850)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKKISLITMILLALVLGMIIGVVLNNTASPETAKLYAQEISIFT
TIFLAUIKMIIAPLVVSTLVVGIAKMGDAKALGRIFSKTLFLFICASLLSIALGLLTV
NFFMPGTGINFVAHGAETTGVVAAEPFFLKVFISHAFPTSIVDAMAHNEILQIVFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamate/aspartate transport proteins (proton glutamate symport proteins) e.g. [Bacillus stearothermophilus] gi|121467|sp|274943|GLTT_BACST percent identity 38 in 416 aa,also similar to C4-dicarboxylate transpor"
                                                                                                                                                                  /product="hypothetical protein"
/protein_id="BAB34182.1"
                                                                                                                                                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                               /gene="ECs0759"
                                                                                                                                                                                                                                                                                                                                                                                AMGAAMVSRWEGEHFGEGCRGKALKPNESNVALP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative transport protein"
/protein_id="BAB34181.1"
/db_xref="GI:13360217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6092. .7372)
/gene="ECS0758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTILLARQAFYBASFELRSAH,QQVASILINDQQASSINDKYVALQLIRNAEVSAKGVLP
MCQDTGTATIYASKGQOIWTGGNDABALSKGIYST QENNLRFSQNAPLDMYTBVNTQ
TNLPAQIDISAVAGDEYHFLCVKKGGGSANKAALVQETKSLLDEKLTAFLLEKMKSL
GTAACPPYHLAFVVGGLSADQTLKIAKLASTKYDNLPTSGNBOGQAFRDIBLEKVLL
EKLEHNPGQYIPASLREENHAQHVQLDLNRPLRDVMQDLARLPVGTRVSLSGPIYVAR
                                                                                                                                                                                                                                                                              /note="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6092. .7372)
/gene="ECs0758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIAHAKIKARLDSGEPMPEYLKHHIVYYAGPAKTPENMACGSLGPTTGGRMDGYIDTF
QAAGGSLVMLSKGNRSQQVTDACHKHGGFNLGSIGGAAALLAQEYVKSLRCLEYPELG
                                                                                                                                                                                                              transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEAVWMMEVENLPAFILVDDKGNNFFSQFEQQHRCASCPAGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="probable transport protein, similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91|120598|sp|P00923|FUMA_ECOLI percent identity 68 in 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="probable fumarate hydratase, similar to fumarate hydratases e.g. fumarate hydratase class I, aerobic (fumarase) - Escherichia coli
       7.29e-18
285.50
56.90%
38.51%
33.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative fumarate hydratase"
/protein_id="BAB34180.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4332. .5984)
/gene="ECs0757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MSKPFIWQEPFLQNKDGTEYTLISDQHITVTELDGEEVIKIAPE"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4332. .5984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVTGRGCHSQILKMADTVSEIRPVKHAFDNGIQAQPGIDW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSTAAFGTVTRAVGHGKTVGVAQYIKGOWDNGEYNLLQPLGVEFHIMGTGFTWETQNR
QADIDAAKEVWSESKRMLADKRYDLVVLDELTYMLAYHYLDTEEVIASLQNRPAQQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="GI:13360216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ECs0757"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative cob(I)alamin adenosyltransferase"
/protein_id="BAB34179.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:13360215"
       Indels:
                            Mismatches:
                                                 Conservative:
                                                                           Matches:
                     297816
67
32
72
                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24510 GCAGACCAGATCTCCATCGTTTCTTACGGTAAAGAAAACCTGCAGTACTGGGTCATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24390 TCTTACAAAGTCACCGTAGAAGGTCACGCGGACGAACGTGGTACTCCGGAATACAACATC 24449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24330 ATCCGTTCTGACTTCGCTCAAATGCTGGATGCACATGCAAACTTCCTGCGTAGCAACCCG 24389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24270 CTGCAAATGCAACAGCTGCAGCAGAACAACATCGTTTACTTCGATCTGGACAAGTACGAT 24329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24153 GCATGTTCTTCCAACAAGAACGCCAGCAATGACGGCAGCGAAGGCATGCTGGGTGCCGGC 24212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
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                                                                                                                                                                                                                             Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, D.C., Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
                                                                                                                                    Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                               Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, D.C. Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D. Genome Sequence of Yersinia pestis KIM J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 ThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis KIM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pestis KIM section 306 of 415 of the complete genome.
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                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 11138)
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/db_xref="taxon:187410"
                                 /strain="KIM"
                                                    /organism="Yersinia pestis KIM"
                                                                                                              Location/Qualifiers
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/function="bhenotype; central intermediary metabolism:
Phosphorus compounds"
/function="bhenotype; central intermediary metabolism:
Phosphorus compounds"
/function="bhenotype; central intermediary metabolism:
Phosphorus compounds

/function="bhenotype; central intermediary metabolism:
Phosphorus 
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177. .517
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to residues 1 to 250 of 250 from E. coli K12: B0755;
residues 29 to 278 of 278 are 89.99 pct identical to
residues 1 to 250 of 250 from GenPept: >emblCAD05220.1|
(AL627268) phosphoglycerate mutase 1 [Salmonella enterica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="enzyme; amino acid biosynthesis: Phenylalanine" /note="DAHP synthetase, phenylalanine repressible; residues 1 to 349 of 350 are 86.24 pct identical to residues 1 to 349 of 350 from E. coli K12: B0754; residues 1 to 349 of 350 from E roli k12: B0754; residues 1 to 349 of 350 from GenPept: >emb|CAD05217.1| (AL627268) phospho-2-dehydro-3-deoxyhaptonate aldolase (AL627268) phospho-2-dehydro-3-deoxyhaptonate aldolase
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FPGHDPRYAKLTDAELPTTESLALTIERVIPYWNDVIKPRIASGERVIIAAHGNSLRA
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/Translation="MMYQNDDLRIKEIKELLPPVALLEKFPSTVNAAETVAKTRNAIH
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GWKGLINDPHMDNSYDINEGLRLARELLVEINDSGLPAAGEFLDMITPQYLADLMSWG
AIGARTTESQVHRELASGLSCPVGFKNGTDGTIKVAIDAINAASAPHCFLSVTKWGHS
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                                                                                              EALLRQLAGAVRARRQ"
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/db_xref="GI:21959964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthase"
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/gene="y3050"
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DAGHMLTDSAALFIALMAVHFSQRKPDPRHTFGYLRLTTLAAFVNAAALLIVILIVM
DAGHMLTDSAALFIALMANHFSQRKPDPRHTFGYLHKGEEKKINVRAAALHVLSDLL
EAVHRFFSPHEVMGTPMLIIAIAGLLANIFCFWILHKGEEKKINVRAAALHVLSDLL
GSVGAMIAAIVILTTGWTPIDPILSVLVSVLILKSAWRLKESFHELLEGAPGEIDIN
GSVGAMIAAIVILTTGWTPIDPILSVLVSVLILKSAWRLKESFHELLEGAPGEIDIN
GSVGAMIAAIVILTTGWTPIDPILSVLVSVLILKSAWRLKESFFHELLEGAPGEIDIN
/**TONTON ON THE STANDARD ON THE STAND
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/function="putative transport"
/note="residues 4 to 310 of 312 are 66.12 pct identical to residues 9 to 313 of 313 from E. coll K12: B0752;
residues 9 to 309 of 312 are 67.44 pct identical to residues 14 to 312 of 312 from GenPept: >9b|AAL19697.1|
(AE008731) putative CDF family transport protein [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4347..5072)

/gene="pnuC"
/gene="pnuC"
/function="transport; transport of small molecules;
/function="transport; transport of small molecules;
/function="transport; transport of small molecules;
/function="residues, purines, pyrimidines"
/note="residues 1 to 238 of 239 from E. coli K12: B0751;
residues 1 to 238 of 239 from E. coli K12: B0751;
residues 1 to 241 of 241 are 100.00 pct identical to
residues 1 to 241 of 241 from GenPept: >emb(CAC89971.1|
(Ad414146) intergral membrane NMN transport protein PnuC
(Yersinia pestis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="t
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ISHATVQMEYQHCGTPDCGINQAAPADGHHRHHHHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="y3050"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="y3051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="residues 1 to 346 of 353 are 82.08 pct identical to residues 1 to 346 of 347 from E. coli K12: B0750; residues 1 to 346 of 353 are 82.94 pct identical to residues 1 to 346 of 347 from GenPept: >gb|AAL19695.1| (AE008731) quinolinate synthetase, A protein [Salmonella trockerstim rmal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="nucleoside/purine/pyrimidine transporter"
/protein_id="AAM86601.1"
/db_xref="G1:21959966"
/translation="MDFLSTGNILVHIPLGAGGYDLSWIEAIGTLFGLLCIWFASKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5194. .6255)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNGSWLWIKSAARNHSRPLSTQG"
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WLSLPKALAWAAVCIAGIYLMTLHIDTVEAWLTRVAVTVWQSLGANVQMPBLOPDAEP
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                                                                                                                                                                                                                                                                                                                                                                      VAHYYTDPEIQALAEETGGCVADSLEMARFGNNHPASTLLVAGVRFMGETAKILNPEK
KVLMPTLNAECSLDLGCPVDEFTAFCDSHPDRTVVVVANTSAAVKAKADWVVTSSIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="quinolinate synthetase"
/protein_id="AAN86602.1"
/db_xref="GI:21959967"
/translation="MSEIFDVNAAIYDFPARPVPLDTNEKAFYREKIKTLLKQRDAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridine nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="y3052"
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/product="tRNA-OTHER"
/note="an+icodo"
                                                                                                                                                                                                                                                             ELIEHLDSLGEKIIWAPDRHLGSYVQKKSGADVLCWQGACIVHDEFKTQALARWKALY
PDAAVLVHPESPQAVVDMADAVGSTSQLIQAAKTLPQKTLIVATDRGIFYKMQQACPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   typhimurium LT2]"
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                                                                                                                                                               LNRMLDFANQLKLQVKGNA"
                                                                                                                                                                                                           KELFEAPTAGEGATCRSCAHCPWMAMNGLRAIAEGLEQGGVMHEIHVDEELRQQALIP
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complement(6725. .6797)

/function="RNA; tRNA"

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RESULT 21
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                                                                                                                                                                                                                           7954 GAAGCAGCCTTTGCTAAAAACCGTCGTGCAGTTCTGGTTTAC 7913
                                                                                                                                                                                                                                                                                                                                                                           8014 GCTGACCAGATCTCTATCGTTTCTTACGGTAAAGAAACCAGCAGTACTGGGCCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8074 GCTTTGGGTGAGCGTCGTGCTAGCGCAGTGAAAATGTACCTGCAAGGTAAAGGCGTTTCT 8015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8134 TCTGACAAAGTTGTTGTTGAAGGCCACGCGGATGAACGCGGGTACGCCAGAATACAACATC 8075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8194 ATCGGTTCTGACTTCGCTCAAATGCTGGATGCACATGCTGCATTCCTGCGTAGCAACCCA 8135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8254 CTTCAGATGCAAGAACTGCAAAAGAACAACATCGTTTACTTCGGTTTCGATAAATACGAT 8195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8296 ------ACAGAGAACGGCAGCAACCTGTCTTCTGAAGAGCAAGCACGT 8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8356 GCTTGTAGTTCCAACAAAAGCGCAAATAATGACCAATCTGGCATGGGCGCGCTGGCACTGGT 8297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8416 ATGCAACTGAACAAAGTGCTAAAAGGGCTAATGTTGGCTTTGCCTGTTCTGGCTGTGGCG 8357
                                                                                                                                                                                                                                                                   159 GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                               139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                               Yersinia pestis strain CO92 complete genome; segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                       AJ414146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThralaargValLeuValAlaGlyHisThraspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="residues 1 to 269 of 269 are 69.62 pct identical to residues 1 to 263 of 263 from E. coli K12: B0742; residues 1 to 263 of 263 are 76.64 pct identical to residues 1 to 269 of 269 are 76.64 pct identical to residues 1 to 274 of 274 from GenPept: >emb|CAC82711.1| (AJ297885) YbgF protein [Pectobacterium chrysanthemi]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAM86603.1"
/db_xref="GI:21959968"
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/gene="y3053"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="anticodon: TTT"
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37.93%
32.87%
                                                                               210050 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prentice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Davis, P., Dougan, G., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Karlyshev, A.V., Moule, S., Oyston, P.C.F., Quail, M., Rutherford, K., Slamonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Genome sequence of Yersinia pestis, the causative agent of plague nature 413 (6855), 523-527 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notce Previously sequenced as Yersinia pestis Yaph /notce Previously sequenced as Yersinia pestis Yaph protein TR:CAC14227 (EMBL:AJ277631) (3705 aa) fasta scores: E(): 0, 99.6% id in 3705 aa. Similar in regions to Escherichia coli Ycha protein TR:Q9JMS3 (EMBL:Ap001918) (1371 aa) fasta scores: E(): 0, 39.1% id in 1405 aa, and to Escherichia coli adhesin Aida-I precursor SW:AIDA_ECOLI (203155) (1286 aa) fasta scores: E(): 0, 29.2% id in 1286 (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015) (2015
ALDLLVNGTAITSGTQGVQSAIQQGGSTVANAIHNYGLASSNSNGDSGLYVNYTLSAI
                                   {\tt GVVTVTDLALNSGTVNITGSGSWDNTDPLATNVSILEQDRAGSTLELINATNVTGDID}
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/strain="CO92"
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AKNDASTAFDROSTVUGATES I VILTNITFALSADNAALIARATIKLISDISTTYTYGAT
DRTLHGLDLNGGTLIFDGSPQSQANGVVTVDDLALNGGT I STTGAGNMENEHPVTP
NVSLLEQDRGD ILLELINAANVGNANNLDLIVDGTAITSGTQGVES ALOGGGSTVAN
ALHNYGLTSSNAGHGGSGLY VNYTLSALELIANGANALLLATESGLTANRVLNAELFGV
GGLVVDAQNGALTLANGNNRYEGTTTYTAGELLILGANGAFGQTSLLNLAAGGASANING
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TRUNINGGDLAVSANTNSGLSGQTGTHADNAAVTLTGTGTLGTSAVEVLGTLKINGANAAM
TNVLSGGGVINTNAAVTLSGNNEFSGAHQIGTDGELTVGQASNIAGASSAFVNLGTLTS
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/initar to Salmonella typhimurium leucine-rich repeat
similar to Salmonella typhimurium leucine-rich repeat
protein Slrp TR:09XCV2 (BMBL:AF127079) (765 aa) fasta
scores: E(): 0, 39.0% id in 644 aa, and to Shigella
flexneri 65.4 kDa antigen IpaH 4.5 SW:IPA4_SHIFL (P18009)
(574 aa) fasta scores: E(): 0, 40.4% id in 589 aa" AFASANDGSTASLSNSTNSYTGTTWVSSGNLRLDADSALGQYTSLLAMSTATHVDINGT
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ANLTSNVLITANGSLGGYGQVTGNVENYGNLINPNALTGGDFGTFTIDGNYTGDEGMI HQIGTDGELTVGQASNLGASSATVNLGTLTSHLILNGVSESIANVLSGVÅGSTVDIIG ASVTLTDTGTLGTSAVEVLGTLNLNGANAAMTNVLSGDGT INTNAAVTLSGNNSFSGA  ${ t TNGGILDLTGGALNLTAGGASTVAGGLTGAGTLNINGGNLSVSAANSGLSGQTHIADV}$ ADRMGETLYTDVFTGEOKTTSLWLRNEGSHNRSRDDSGELKTQDNRYVMQLGGDVAOW SRNAQDLWRVGVMAGYANSSSSTVAQVAGYRSTGSVDGYSVGIYGSWLADNADDTGAY NIGTLAMNGGTLLFDNIVDNAGIITSDGTIAANSINTTGGGEVRVNLPSNLAPSLDGL SVMELDEGEIIVTLATGAATGTGHELTLTDENGDPISAVTXQGYHNAGSTSAAATGSF complement(12049 .13929) /gene="YPO1005" VDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGESVNQSYFIQPKAQVVWMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKAKVSGPAFKEFVEANWIH TENTILAGDTSVTDRLVITGDTAGQSVYTVNNIGGVGARTFEGIKIIDVGGDSAGQFT LNGRAVGGAYEYFLYQGGASTPDDGNWYLRTEADDRRPEPASYTANLAAANNMEYTSL NYGMTTGEDYDGLYVNYGLTALELLSTGSEALVLTAILANNGTQSNDLSAQITGSGDL complement(12049. .13929) LGVKYNF" QLENTAREKVKTLKTLNYNSVDDTEVTLAYQVKLLNSLQLSSVNKEMRFFGVSHVTAD DLLSAETRVKTAENQDFSRWLSOWSPWKSVVQRTEPERYAAAVEKQYHALENTYPDKL SVTSNOLTQLPETLPASLSFLMYLSNRLTKLPENLPGSLRCISAEYNQLSOLPDLARL PQNCEILLEGNPLSTSTLQVLQHLRINPYYOGPRINWSELDNLPPASLRNIVATMLPP EQQNRLAGDWANIETEANSAAFSVFLHRLATTQNANNIPEFKOQIAAWLLQLADSPTL LPATLPDNIQKLNASFNQLRTLPDTLPASLLSLNVYGNELERLPESLPEGLKELDVND NESLQLPNRLPPNLESLGIASCGLTELPTLPNSLKRLDADSNQLRTLPDTLPISLLNL /db_xref="SPTREMBL:Q8ZHA0"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                            152592 GCTTGTAGTTCCAACAAAAGCGCAAATAATGACCAATCTGGCATGGGCGCTGGCACTGGT 152651
                                                                                                                                  152532 ATGCAACTGAACAAAGTGCTAAAAGGGCTAATGTTGGCTTTGCCTGTTCTGGCTGTGGCG 152591
41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                        21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                              1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-*Similar to neighbouring CDSs vpO1005 and vpO1007.
/note-*Similar to regions of Salmonella typhimurium secreted
Similar to regions of Salmonella typhimurium secreted
protein h2 TR:Q9RPHO (EMBL:AF160727) (788 aa) fasta
scores: E(): 2.5e-24, 41.9% id in 272 aa, and to regions
of versinia pestis outer membrane protein YopM TR:068701
(EMBL:AF053946) (409 aa) fasta scores: E(): 7e-23, 40.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(13099. .13164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Pfam match to entry PF00560 LRR, Repeat, score 17.30, E-value 0.36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat, score 10.40, E-va complement(13468. .13539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat, score 12.80, E-value 8.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(13219. .13290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat, score 9.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat, score 12.90, E-va complement(14492. .15367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(13294. .13353)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00560 LRR, Leucine Rich Repeat, score 9.30, E-value 44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="YP01005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00560 LRR, Repeat, score 15.40, E-value 1.3" complement(14732. .14791)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDPRTVAGEORGOAVARMKECLENNAERLNLSSLDLTSLPDTLPPCNELNIICNNLTE
LPTTLPDNLQTLKASYNOLRTLPNTLPASLLSLKVHMNELERLPEPLPEGLKTLDVGC
NTSLOLPSRLPPVLESLDISNCNLTELPTLPNSLKELDAHGNOLRILPDTLPISLLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative antigenic leucine-rich repeat protein"
/protein_id="CAC89849.1"
/db_xref="GI:15979075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(14492. .15367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00560 LRR, Leucine Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(13543. .13602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="pfam match to entry PF00560 LRR, Repeat, score 10.40, E-value 30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="YP01005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Pfam match to entry PF00560 LRR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="YP01005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(14657. .14728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  id in 259 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="YP01006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="YP01006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="YP01005"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVAYNQLTALPENLPGSLRCIYTEYNQLSQLPDLAHLRQNCNICLDGNPLSPSTLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MYLSNITSNVSMPNIGPDREIHADRPAATALTPADYHAIWEKWE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat, score 9.30, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="YP01006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:Q8ZH99"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00560 LRR,
Repeat, score 9.30, E-value 43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="YP01006"
                                                                                                                                                                                                                                                                                        56.32%
37.93%
32.87%
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Matches:
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Indels:
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Always, C. C., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camaryo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M. IT., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B. N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Fakita, M.A., Tamura, R.E., Texeira, E.C., Tezza, R.I.D., Trindade dos Kitaiima, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152994 GAAGCAGCCTTTGCTAAAAACCGTCGTGCAGTTCTGGTTTAC 153035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
         da Śliva, A.C.R., Ferro, J.A., Reinach, F.C., Farrah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.F., Alves, L.M.C., do Amarral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarrotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Farla, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite, Jr., R.P., Lemos, B.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Martins, E.C., Machado, M.A., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Mura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,
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AE012414.1 GI:21114710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comparison of the genomes of two Xanthomonas pathogens with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differing host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas campestris pv. campestris str. ATCC 33913. Xanthomonas campestris pv. campestris str. ATCC 33913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSSI,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                             'translation="MLQRLERDYGLKHRSGTSYMRGGVCPACSKKELYTFEPKPWYIK
GREAKKGHELIVKDLYDDLFDDWSKRFPMTQASPTASADAYLESSRGFALAPLRGLY
TQESYYDIKVKEGTATYFFALDKGGWEFLIDRPHRFGKOKAFFAPGKYAGAWKCAP
AAAELMRTATEYWIVEGIFDAIALLQHGVCAVSAMSCNAFPDESIRQLKYLAGAWLLPT
LVWGLDNEPGAEDYTHHHARRADALGFNSRAALIAQPYTGKKIDWNDLHLRAQAGGDS
                            FPHDANSVKGTFTGGHISSASEFKKRLISLAAGAMFTGSGHQLDÄLIEEQTEAIKTVE
AIDFVGYSKEHRAYLLGDIAVRDGEVVTANEEDYFSFKKLRLKSTQKSIRLEIQRDPE
                                                                                      QKQWDAALTEARYQGDLLMARSAIEKGLLMYDHNQASDFWLEYRSRLYWFEFDTYRFE
KLLRDYEPEEDSEIDPDKLAKIRRAACSVNKIANCYPEALYFQRQEVTDESWYYFRID
\mathtt{AFRMDWLPWLWQCFGTHGMVAMTFWFGSLFAEQIRAGHKSFPFLEATGEAGAGKTTLL}
                                                                                                                                                                                                                                                                                                     /product="phage-related protein"
/protein_id="AAM42274.1"
/db_xref="GI:31114214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHLASGGAYEVITTPRPIGKSLAALALRSTVRKGG"
                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="orf37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="XCC3002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="orf37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MSQSNGWATAQAPRFVDAPSQASQQYVAPHKKREQADVLRLQVE"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:21114213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="AAM42273.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MAQLMLRGLLMSSRTHSMHALATDAAMELLDYGSVAREISA"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="AAM42272.1"
/db_xref="GI:21114212"
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/protein_id="AAM42271.1"
/db_xref="GI:21114211"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="ATCC:33913"
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ERVIKNHAOMIALLDCLRMVITIPEEMIKATRDALLEMAFEROKAISADHAQVNEFWE
VYEYLEATGNGKPVVNHSRDASRIAININQFAAKAAQFSQVVPDIKVLRGILADSRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="XCC3003"
4103. .4327
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ELKDFFGGGTLATRGVRNGGNDTYEPFFRGTTVISQNAAVDASEAILTRIVKLHFKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLVSANTAVNSAVLTNGFGAGTTVKCWVFSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="XCC3006"
5090. .5245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THDAVVVVAALTMGQHAVTRSQISSAGPGQEATTPVEAAFDLAVGKDCSAIATLYITHDAVVVVAALTMGQHSSAAQRWERRRGPGKGWKLISGPRLFTSEAHRISNALAKFMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGISHDGIAAVADFMREELLDIACNARHVREPTKPPTGADLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="AAM4276.1"
/db_xref="Gi:21114216"
/translation="MNSVRATAYPEDADYTISEEEHDRLWRVQQAASLLATLNHDIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MMQGYVLAMLHSDAQHDVAPVLIACEATGFDDVLLGGDAHSVVL/
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/protein_id="AAM42275..
/db_xref="GI:21114215"
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                                                                                                                                                                                                                                                                                                                               /gene="XCC3007"
5238. .5513
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/protein_id="AAM42277.1"
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/protein_id="AAM42278.1"
/db_xref="GI:21114218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11/
                                                                                                                                                                       /product="conserved hypothetical protein"
/protein_id="AAM42279.1"
/db_xref="GI:21114219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="XCC3006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:21114217"
                                                                                                                                /translation="maesivvygpmasgkslnaeaicqayglkrvvelderlqrkged
wqlsqndvymltndqalaertaqrmrvktvaitearlrvgaamralr"
                                                                                                                                                                                                                                                                               note="putative; ORF located using Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                        /gene="XCC3007"
                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MIAPTIGGALLYRLWISRPTRTAHIGLAVGQIPQRLRRRRAMAV/
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/note="putative; ORF
/codon_start=1
                                             /gene="XCC3008"
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                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                           126 ValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIle 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
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da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,J. Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,
                                                                                              xanthomonas axonopodis pv. citri str.
xanthomonas axonopodis pv. citri str.
Bacteria; Proteobacteria; gamma subdiv
                                                                                                                                                               AE011958.1 GI:21109461
                                                                                                                                                                               the complete genome. AE011958 AE008923
                                                                                                                                                                                                            Xanthomonas axonopodis pv. citri str. 306,
                                                                                                                                                                                                                                 AE011958
                                                                                 Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAC---GGCCCGGGCGACCTG---GATACCGATGCTTGCCTGCGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---CAGCGCGTTGTCTACTTCGATCTGGATCAGGACTCCCTGAAGCCGGAATTCCAGGCC 10609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLys 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerThrSerGlnValMetValAlaProAsnAlaProThrGly---TyrThrGlyValIle 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys
                                                                                                                                                                                                                                                                                                                                                                                       SerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsn 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                                                                                                                                            ArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                               CGCCGCGTCGAGATCGTGTAC 10348
                                                              bases 1 to 11713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="XCC3009"
5932. .602/
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/db_xref="GI:21114220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical protein"
/protein_id="AAM42280.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MLNRHDWLADMDYTIAQALDRIDEDTTAHLRQAERAIRNGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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276.50
55.09%
37.72%
32.11%
                                                                                                                                                                                                                                  11713 .bp
                                                                                                  gamma subdivision;
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Matches:
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Indels:
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306
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63
29
60
15
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                                                                                                       Xanthomonas
                                                                                                                                                                                                                     29-MAY-2002
of 469 of
                                                                                                        group;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira, JT., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teikeira, E.C., Tezza, R.I.D., Trindade dos Katta, M.M., Tuffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Katta, H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade de Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brazil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTHYLPTSTGFVEAAARELGWCLAPEAMVLPAVRNRQVVIIDPTRWLDVPLYWQYTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGQVLVMRTAPCRPTPAGERLLRRLKPMQVLEAEAVADLLPGDRIAGHPRTLATAVND
DSLQTWFLQALSSLHRAHGFLFDVQMDDQDHTLELLRAGSVLGAVTSERAPLQGCNVQ
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/protein_id="AAM37980.1"
/db_xref="G1:21109463"
                                                                                                                                                                      /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                 complement(1258. .1617)
                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1258. .1617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSNALQQLSQALRKAAATSLRGSR"
                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                 /note="XAC3135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="transcriptional regulator lysR family'
/protein_id="AAM37979.1"
/db_xref="G1:21109462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark"
                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MDLLHPQLAAFAAVLNEGSFDAAAQRLALTPSAISQRIKALEDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="XAC3134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="XAC3134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pathovar: citri"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Xanthomonas axonopodis pv. citri str. 306"
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complement(4662. .5480)
/gene="XAC3140"
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                                                                                                                                                                                                                                                                                       complement (4662.
                                                                                                                                                                                                                                                                                                                                                                /translation="MNAAAVPSETVQSPLPRLKITEIFLSLQGEAEAAGWPTVFVRLT
GCPLECHYCDTAYAFHGGQWHDIDAIVAEVASHGVRHVCVTGGEPLAQKRCLVLLQKL
CDAGFDVSLETSGALDVSAVDSRVSRVVDIKTPASGEEARNRWENLPLLTARDQIKFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="radical activating enzyme"
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/db_xref="GI:21109466"
                                                                                                                                           /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                         LLWNDEPGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3936. .4619)
/gene="XAC3139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3936. .4619)
/gene="XAC3139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="two-component system sensor protein"
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/db_xref=="701:21109464"
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IFTPVFGPDGKVEAIAGATRDITEHKQHEQHLQLLINELNHRVKNSLVMVQSILARQSF
TNAGSLGDAQEKLDARLLALSRAHDTLTRENMVSADILELTROAAALYESHDGQRFTL
QGDSCRLDPRRALALSMALHELCTNALKHGALSLPAGNVLVSWERSTRGEQELLELIN
                                                                                  /transl_table=11
                                                                                                                                                                                                                                                               /gene="XAC3140"
                                                                                                                                                                                                                                                                                                                                        ICSRADYEWSREIVAAHALDRRCTVWFSPSKSEVSPRQLADWIVADRLPVRFQMQLHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAARVAAAQGVIAHKVVDVDLRSIGGSALTDDIEVPDAGGDGIPVTYVPARNTINLSL
ALGWAEVIGANDLFCGVNAVDYSGYPDCRPEFVRAFEVLANLATKAGVEGAGLRVHAP
                                                                                                                codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3618. .3693
/gene="XAC3138"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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/db_xref="GI:21109465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="XAC3138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQFLSKADIVREGVRLGVDFGVTVSCYRADADGRACGHCDACRLRAAGFADAGIPDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKKAVVLLSGGMDSAAVIALAQEQGFAVYALSVRYGQRHTSELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="identified by sequence similarity;
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="exsB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="exsB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="identified by sequence similarity; putative;
located using Blastx/Glimmer/Genemark"
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agnldlalldinlggtlsfpiaeeldargvpyifvtgyaqggiperyrhrhglqxpfh
frdlxhalsllqhrsae"
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translation="MRFRVTSLFVAAALVVAAPAYAQRASLADRVAVLEQQQANSQAN/

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5975 TCCCTGCTGTCCGTTGCTGCTGGCTGGCTGCTTGCTCGAAGAAGGTGAAGGAAACTCCGCCC 5916
                                                                                                               5915 CCTGCGACCGATACCACCGCTGGTTCCTCGGTTCCCACCGGCCCGTCCACCTCTGGCCTG 5856
                                                   106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
                                                                                                                                                                                                                                                                                                                                                                                                      46
                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys------
                                                                                                                                                                                                                                                                                    66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerThrSerGlnValMetValAlaProAsnAlaProThrGly---TyrThrGlyValIle 45
                                                                                                                                                                                                                                                                                                                                                TAT---GGTCCGGGCGACCTG---GATGCCGATGCCTGCCTGCGT----
                                                                                                                                                                                                                                                                                                                                                                                                   TyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLys 65
IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                                              ---CAGCGCGTTGTTTACTTCGATCTGGATCAGGACTCCCTGAAGCCGGAATTCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDLLNQLQQARSDLQALRSTVEQLQHDNEQLKQQSKDQYLDLDGRLNRLEGAGGATPP
LPARIGNVTPAAPAARPAAAATSEKPPTVHGDPGTLAVSNDERTAYNVAFDALKNGK
YDDASQLFLSFLELXPNGVTTPNALXWLGESYKATRNFQLABAQFRDLVSRYPTHDKA
AGGLLKLGLSQYGEGKNNEAQQTLQQVASQYPGSDAARVAQERLQSIRLGQQLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6063. .7382)
/gene="tolb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAQSLHRYPMNKSTRVLLVSLLSVAVLAGCSKKVKETPPPATDT
TAGSSVPTGPSTSGLYGPGDLDADACLRQRVVYFDLDQDSLKPEFQAIMACHAKYLRD
RPSSRITLQGNADERGSREYNMGLGERRGNAVSSSLQAAGGSASQLTVVSYGEERPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVRGAFWTRIAYVTASGKGGAMRYALMVADSDGYNPQTIVRSAEPLLSPNWSPDGKKL
AYVSFERGNSSIYLQDIATGARELVSSFRGINGAPSFSPDGRRLALALSRSGNPEIYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Tolb protein"
/protein_id="AAM37986.1"
/protein_id="AAM37986.1"
/db_xref="GI:21109469"
/ta_sref="GI:21109469"
/ta_sref="GI:2110
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/protein_id="AAM37985.1"
/db_xref="GI:21109468"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDLGSKQLTQLTNHFGIDTEPTWAPDGGSIYFTSDRGGRPQIYQVAASGGSANRVTFQ
GNYNATASVSFDGKKIAVAQGSGNTYRIAMMDRSLGSPSWSTLSPGSLDESPSFAPNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
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/note="XAC3142"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeuchi, C., Yamada, M. and Tabata, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 7 (6), 331-338 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (E-mail:kaneko@kazusa.or.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11214968
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complement(54. .1655)
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/codom ~*
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                                       complement(1719. .2894)
                                                               /gene="ml13876"
                                                                                          complement(1719. .2894)
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126 ValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIle
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AP003003 BA000012
AP003003.2 GI:14024067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:http://www.kazusa.or.jp/rhizobase/,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
On May 11, 2001 this sequence version replaced gi:11994978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete genome structure of the nitrogen-fixing symblotic bacterium Mesorhizobium loti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTACGGCGAAGAGCGTCCGGTCTGCACCGAGTCGAACGAGTCCTGCTGGTCGCAGAAC
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                                                                       VATPHLGASTAEAQENVALQVAEQMSDYLIKGĀVSNAINMPSITAEEAPRLKPPVKLA
EVLGAFVGQVTEDPIMEVEILFDGSTATMNTRALISATLAGLIRPQVSDVNMVSAPIM
VKERGIIVAEVKRDKSGVFDGYIKLTVKTEHRFRSIAGTCFSDGKPRFIQIKGINLDA
EVGQHMLYTTNADAPGIIGLLGTVCGENGVNIANFQLGRNRPGGDAIALLYLDAPFPE
KVLEQVRAHKSIDSAKRLQFDVGGI"
                                                                                                                                                                                               RGVGLKMHVVAFDÞFÍSDKRAEELGVEKVELDELFARADFITLHTÞLTDKTRNIIDAG
AIAKMKNGVRIINCARGGLIVEADLIAALKSGKVAGAGIDVFEVEPABQNALFGMENV
                                                                                                                                                                                                                                                                  OYDGLAIRSATKVTEKLINAATRLKVIGRAGIGVDNVDIPAASRKGIIVMNTPFGNSI
TTAEHAVAMIFALARQIPEANASTHAGKWEKNRFMGVEITGKTLGVIGCGNIGSIVAT
                                                                                                                                                                                                                                                                                                                                                  /product="phosphoglycerate dehydrogenase"
/protein_id="BAB50672.1"
/db.xref="GI:14024068"
/translation="MAPRVLVSDKLSPTAVQIFKDRGVEVDYLPDLGKDKEKLLEVID
/translation="MAPRVLVSDKLSPTAVQIFKDRGVEVDYLPDLGKDKEKLLEVID
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gene CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLAGGGVVSTVMSNLGLERFLGDMKLQLHRTKVGDRYVVEHMRAHGLNVGGEQSGHIV
LSDFSTTGLGLVSALQVLACIKRQGRPVSELSKKFEPVPQLLKNVRIAGGKPLEEAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="phosphoglucomutase/phosphomannomutase family protein; MrsA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ml13879"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGWYLRGDVSYLAQKSFKNDDFAFTPASFDEKEDPIFASIGFGYHFNDYLRADLNLG
YLPGNKIGIGYDDSLSVVPPATSTVASADLKNYAYSLMLNAYVDLGTYVGITPYLGGG
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   AGGKGLTMAECSAKYQAAKTANTLKGQKWNDFRKAECGAAAADDDSVPAPSEANYTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADRKGLTICDATSAAFAQRLDFEKLDVVTFSWQKVLGGEGAHGMLILSPRAVARLESY
KPAWPLPKIFRLTSGGKLIEGIFKGETINTPSMLCVEDYLDALHWAKSIGGLDVLVAR
ADANAAVLDGFVDKSSWLGHLAVQPATRSNTSVCLSFTDPDVAALDADGQATFAKGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="phosphoserine aminotransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(5193. .6545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIQGGRMFEWDASSAGPGFDRGINTHEVRGGLRYQFGGNNGCAAPVVAYQPEPEPIYT
K″
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4111. .4944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SALDKEGVAYDIGSYRDAPPGLRIWCGATVETSDLETLLPWLDWAFAAQKASLKAAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="mll3878"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTLTSRIVLALAGIGLLPLTPAVAADYDPPIYADQAPDYVPVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB50674.1"
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/transl_table=11
Pred. No.:
Score:
                                                          Alignment Scores:
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cns

gene

4.45e-16 269.50

Length: Matches:

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SLELPSLFGDKKKPDQVQFAQOSNGAGATGLEDQLRQWNGKIEELNFQILOMQEQMRK
QQEDNEFRFQQLEGGAQGGQPPAPKKSDATTNTNTDVAAAPATQAPADAGAAPGGNQS
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                                                                                                                                                                                                                                                                                                                                                                                           HSAD"
                                                                                                                                                                                                                                                                                                                                                                                                            QAFENLGLPQGEPRLPVFAARPVVSPFARFLPSFDLAPARAVAELIGASPLPASPLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   AVDNTIWDGRRHITLNDMSGALLIAPLGAAAARRLAIDDGETPASLIRAALAAEPTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                deaminase-related protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Similar to YaeN protein [Bradyrhizobium japonicum], contains similarity to cell cycle protein MesJ/cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(10675. .12039)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSLFGYLISWLPMILILGVWIFFMRQMOSGSGRAMGFCKSKAKLLTEAHGRVTFQDVA
GVDEAKEDLEEIVEFLRDPQKFQRLGGKIPRGYLLVGPPGTGKTLLARSVAGEANVPF
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                                                                                                                                                                                             transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILTKKKKEWIALAQGLLEYETLSGDEIKQLIAGEKPARDLGDDTPPSRGSAVPKSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTRWGFSDKLGHVAYGDNQEEVFLGHSVARTQNISEETAQIIDAEVRRLIDEAYSTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVAAGRVKTVTIAGARITGTYTDNSTGFQTYSPGDPQLVSRLQDKNVTINARPEADGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(8624. .10552)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8624. .10552)
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8079. .8537
                                                                                                          translation="MHLRSVLSGTLAALLLSGFTALASGPGASGPGQSTDSGFSFHLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="metalloprotease (cell division protein); FtsH"
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GFYSLCNAKLKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNPNYRNLALWAIIAVLLIALFNLFQTPQTRGASSDVPYSQFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                       MEDLINE
                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                          TITLE
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                                                                                                                             PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                  Simpson,A.J., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M., Alvarenga,R., Alves,L.M., Araya,J.E., Baia,G.S., Baptista,C.S., Alvarenga,R., Alves,L.M., Araya,J.E., Baia,G.S., Baptista,C.S., alvarenga,R., Alves,L.M., Briones,M.R., Baross,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R., Bueno,M.R., Camargo,L.E., Carraro,D.M., Carrer,H., Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C., Costa-Neto,C.M., Coutinho,L.L., Cristofani,M., Dias-Neto,E., Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J., Ferreira,V.C., Ferro,J.A., Franca,S.C., Franco,M.C., Frohme,M., Furlan,L.R., Garnier,M., Goldman,G.H., Goldman,M.H., Gomes,S.L., Gruber,A., Bo,P.L., Hoheisel,J.D., Junqueira,M.L., Kemper,E.L., Kitajima,J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xylella f
AE004009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xylella fastidiosa 9a5c.
Xylella fastidiosa 9a5c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE004009
Simpson,A.J.G., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M., Alvarenga,R., Alves,L.M.C., Araya,J.E., Baia,G.S., Baptista,C.S., Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.S. Bueno,M.R.P., Camargo,A.A., Camargo,L.E.A., Carraro,D.M.,
                                                                                                                                                                          Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                          The genome sequence of the plant pathogen Xylella Xylella fastidiosa Consortium of the Organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE004009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCGCGGCACGCGCGAATACAATCTGGCGCTCGGCGCCGCCGCCGCCGCCGCCGCCGCCGC 13568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGCCCGGCTCGGCGCAGGACTTCACCGTC------AACATTGGCGACCGC 13748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CCGAACAACGCCGCCGACCTCGGCCTCAACGGC------GCCGGTGCGGCA 13793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValAlaProAsn-----AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGCTGGTGGCGATGCTCGCCATCGCCGGTTGCGCTTCGAAGAAGACG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSerGlnValMet 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGCGCAGTGGCTGAACCAGTACAAGCAGTACGCCATCGTCGTCGAAGGTCACGCCGAC 13628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACGTCCGGTCGCGGTCTGCGACGACATCTCCTGCTGGTCGCAGAATCGCCGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 10833)
                                                                                               (bases 1 to 10833)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fastidiosa 9a5c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE003849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.97%
40.25%
31.30%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10833 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-349116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obstacle of 229 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
53
57
                                                                                                                                                                                                                                    for Nucleotide
                                                                                                                                                                                                                                                            fastidiosa. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 15-JUN-2001
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gene
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Nascimento, A.I.T.O., Netto, I.E.S., Nhani Jr.A., Nobrega, F.G.,
Nunes, L.R., Oliveira, M.A., de Oliveira, M.C., de Oliveira, R.C.,
Palmieri, D.A., Paris, A., Peixoto, B.R., Pereira, G.A.G., Pereira
Jr., H.A., Pesquero, J.B., Quaggio, R.B., Roberto, P.G., Rodrigues, V.,
de M. Rosa, A.J., de Rosa Jr., V.E., de Sa, R.G., Santelli, R.V.,
Sawasaki, H.E., da Silva, A.C.R., da Silva, F.R., da Silva, A.M., Silva,
Jr., W.A., da Silveira, J.F., Silvestri, M.L.Z., Siqueira, W.J., de
Souza, A.A., de Souza, A.P., Terenzi, M.F., Truffi, D., Tsai, S.M.,
Tsuhako, M.H., Vallada, H., Van Sluys, M.A., Verjovski-Almeida, S.,
Vettore, A.L., Zago, M.A., Zatz, M., Meidanis, J. and Setubal, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-Dorry, H., Facincani, A.P., Ferreira, A.J.S., Perreira, V.C.A., Ferro, J.A., Fraga, J.S., Franca, S.C., Franco, M. Ferro, V.C.A., Ferro, J.A., Fraga, J.S., Franca, S.C., Franco, M. Fromme, M., Fullan, L.R., Garnier, M., Goldman, G.H., Goldman, M.H., Gomes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Kitajima, J.P., Krieger, J.E., Kuramae, E.E., Laigret Lambais, M.R., Leite, L.C.C., Lemos, E.G.M., Lemos, M.V.F., Lopes, C.G., Machado, J.A., Machado, M.A., Madeira, A.M.B.N., Madeira, H.M.F., Marino, C.L., Marques, M.V., Martins, E.M.E., Martins, E.M.E., Matsukuma, A.Y., Menck, C.F.M., Miracca, E.C., Miracca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and Applyers. Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Bioinformatics Lab -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOLEYARGLITTPEMEEVAIREQQREEQTVENLRGQREAGDAWGALVGTPITPEEVVRD EIARGRAILENNINHPESEPMIIGRNELTKINANIGTSALSSCIAEEVEKLVWAIRWG ADTIMDLSTGROIHATREWILRNSPVPVGTVPIYQALEKVGGHVEALSWAVFRDTLIE QAEQGYDYVTYHAGVLLEDFIPITASRKITGIVSEGGSIMARWCQAHRSEBRETTTTFELL CEIMRAYDVAFSLGDGLRPGCIADANDAAQFAELEILGELTHIAWNHQVQVMYEGPGH VPMHLIKANNDXQLAACGEAPFYTLGFLTTDIAFGYDHITSAIGAAMIGWYGTANLCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment coverage: 91.4 %/subject alignment coverage 97.5 %); identified by sequence similarity; putative; located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVTAPLLGARKIYITGSRQDIRVPMREIALTPSSARYGGNENLSLALYDTSGIYTDPQ
ATIDLACGLPRLRAAMIDERADTVEAALYFKVPESVSVTAPPFPTAPRPRRARDNVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="XF1888"
192. .2081
                                                                                                                                                                                                                                                                     /note="similar to SP|Q44532 (percent identity: 59 %/que: alignment coverage: 97.3 %/subject alignment coverage: 97.7 %); identified by sequence similarity; putative; 01 located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTPKEHLGLPNLQDVHDGIIAYKIAAHAADLAKGHPAAQARDDALSKARFEERWQDQF
HLSLDPEKALALHDESLPKEAHKRAAFCSMCGPQFCSMKISQEVRDASSNELSDGNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="thiamine biosynthesis
/protein_id="AAF84694.1"
/db_xref="GI:9106981"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xylella fastidiosa 9a5c"
/db_xref="taxon:160492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .10833
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/product="ferredoxin-NADP reductase"
/protein_id="AAF84695.1"
/db_xref="GI:9106982"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2213. .2992
/gene="XF1889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="XF1889"
2213. .2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MDRAARPPWQRRKVPRRREVPSLSGRTIVNITTALPLPTHLLSE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11/
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                                                                                                                                                                 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Franco, M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campinas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lopes, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            59 %/query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .н.ѕ.,
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CDS

TEARPLLRAYSIASANWEEQLEFLSIKYQNGLLTSRLQHIKPGDKILVGKKPTGTLLI HDLHPGRHLYLLGTGTGLAPWLSIIKDPETYERFDKVILTHGVRYSKDLAYRDYFEKE LPQHELLGETIRKKLLYYPAVTREDFPNRGRLTHLIESGAMQNTLGLPIIDQANDRFM

translation="MSPAFGTETVIHVHHWTDAYFSFITTRDSGFRFENGQFVMIGLE/

FEATURES

TITLE JOURNAL

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CDS
                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                       alignment coverage: 98.8 %/subject alignment coverage: 98.4 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTGIRMALTLYIVTOFFDGNIGEGNANSTYGAYLALVYASAIFGGFIADRIIGYQ
RSIIIGAVIMACGLELITVPSRTMFEIGLATIVIGNGLEKPNISSLVQQLYABGDTRR
RSIIIGAVIMACGLELITVPSRTMFEIGLATIVIGNGLEKPNISSLVQQLYABGDTRR
RROTIFYMGINAGSLISPLITSWLAGQVFGTPMQQNYKVVFIASGIGMFLSLLWFWI
GKRQLKGIGLPFKDGESIFRTFLIIFGVLAGALAIFDAYLLLAKLMATTLAWILGLLFAAL
ATLLIVTALRNGXIQRDRVIAMLIIFVFNVEYMMFFEQAGSSENFLAKNIVDRQILSN
WEFPVGWFQSVNPLAIILLAPIIAVIWSLLDKYRIEPSIPRKFSLGLWFNGFGFLILM
YALSNLLMASNMIPFWSLIAVYVIQTVGELCLSPIGLSMVTKLAPVRLVGFAMGGWFL
STAIGNNLSGVFASFVSGEEGMTVSSALRGYTFGFWSLIGSGILLFLISPLINRLMHG
                                                                                                                                                                                                                                                                                                                                                                                              RIVLKDDLNLLSEPTLLAGFDVGFEDEGRTTRAAAVLMNACDLKLLETHVVRVPTSMP
YVPGLLSFRELPALLQALTQLSRIPALVFVDGHGIAHPRRLGIAAHFGLVTNLPCIGV
AKKRLVGDFVEPGTAFGEHTPILLHGTQVGWALRSKIRCKPLMISPGHKISLHSALTW
                         /product="phosphoglyceromutase"
/protein_id="AAF84699.1"
/db_xref="GI:9106986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to SP|P32679 (percent identity: 53 %/query alignment coverage: 83.1 %/subject alignment coverage: 94.6 %); identified by sequence similarity; putative; ORF
/	ext{translation="MTRKLVLLRHGQSQWNSMNRFTGWVDIGLTEQGHQEATMAGHLM}}
                                                                                                                                                                                                          /note="similar to SP|P31217 (percent identity: 56 %/query alignment coverage: 98.8 %/subject alignment coverage:
                                                                                                                                                                                                                                                                                                                                                                                TQRCLNGYRLPEPTRQADRLASRRGQKIVSDLPSLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="endonuclease V (deoxyinosine 3'endonuclease)"
/protein_id="AAF84698.1"
/db_xref="GI:9106985"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="XF1892"
complement(5578. .6342)
                                                                                                                      /transl_table=11
                                                                                                                                            codon_start=
                                                                                                                                                                                                                                                                             /gene="XF1893"
                                                                                                                                                                                                                                                                                                                                   /gene="XF1893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MPVYALISDTGMMVFMKISSIDSIFAGWDGSITEARRLQSDMAE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (5578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"similar to SPIP94408 (percent identity: 35 %/query alignment coverage: 96.7 %/subject alignment coverage: 100.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="di-tripeptide ABC transporter membrane protein"
/protein_id="AAF84697.1"
/db_xref="GI:9106984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  located using Glimmer/RBSfinder"
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RGQVLLLVMVASRCGGTPQYAGLEMLWQRYRDAGLIVIGFPCDQFAGQEBGDEAKIAE
FCTLNYGVDFPMAAK.KVNGADAHPLWQWLKHRRRGLFGMAAIKWNFTKFLIGRNGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSVDTTVKNTVYLATPPTQLPKFETIFGHPKPLWMLFMAEFWER/
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protein_id="AAF84696.1"
jboxref="GI:9106983"
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DEFINITION Sequence 178 from patent US 5994066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9037 GTTCTTGGTTGCCATGCAAAATATCTTCGCAACCGTCCCTCTGCACACATCACATTACAG 8978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9190 CCAACTGTTTCTACGCCCGCACCCACCACTACGGCGCCAACCGATTCTTCTGGG---CTT 9134
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                                                                                                                                                                      166 ArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                      126 ValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIle 145
                                                                                                                                                                                                                                                                             146
                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 ------AlaPro-----AsnAlaProThrGlyTyrThrGlyValIle 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 MetThrGlyCysAlaAsnLysSerThrSerGlnValMetVal------
                            AR089419
                                                                                                                                                                                                                                                           SerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsn 165
                                                                                                                                                                                                                                                                                                                                                                                                          GGCAATACTGATGAGCGCGGTTCGCGTGAGTATAATATAGCTCTGGGTGAACGGCGCGGT 8918
                                                                                                                         CGGCGCGTTGAAATCGTCTAT 8777
                                                                                                                                                                                                                  AGTTACGGTGAAGAGCGTCCGGTTTGCACTGAATCAACAGAAAGTTGCTGGTCACGTAAC 8798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLys 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mndorhunrlmnatrsolkiseiflsloggeansvgwptvfvrlt
GCPLRCQYCDTAYAFHGGEWCSIDTIVSEVRSYGVRHVCVTGGEPLAQKRCLLLLEKL
CDAGFEVSLETSGALDIAAVDLRVSRVVDIKTPGSGEAHRNHWPNLALLTPHDQIKFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
/protein_id="AAR84700.1"
/db_xref="GI:916987"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                      451
                                                                                                                                                                                                                                                                                                                                                                                                                         170 LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergeron, M.G., Picard, F.J., Ouellette, M. and Roy, P.H. Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories patent: US 5994066-A 178 30-NOV-1999;
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                                                 Deich,R.A., Metcalf,B.J., Finn,C.W., Farley,J.E. and Green,B.A. cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton protein from Haemophilus influenzae
                                                                                                                                                                              lipoprotein; outer membrane lipoprotein.
H.influenzae (strain S2, sub-species Rb)
Haemophilus influenzae
                                                                                                                                                                                                                                                                                        H.influenzae PC protein (15kd
                                                                                                                                                                                                                                                                          membrane lipoprotein), complete cds.
                                                                                                                                                                                                                                                                                                               HEAA15KLP
                   88115138
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                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                           Sequence 3 from Patent WO 106718
                                    Unclassified.
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QQRYNTYYFGFDKYDITGEYYQILDAHaaylnatpaakylvegntdergtpeynialg
QRRADAYKGYLAGKGYDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY"
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/protein_id="AAA24940.1"
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/db_xref="taxon:727"
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AUTHORS

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Deich,R.A., Zlotnick,G. and Green,B.
VACCINES AND DIAGNOSTIC ASSAYS FOR HAEMOPHILUS INFLUENZAE
Patent: WO 8804932-A 2 14-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                Sequence 2 from Patent WO 108799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Draft entry and printed copy M.B.Nelson, 27-MAY-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lipoprotein; outer membrane protein.
H.influenzae (isolate 1479) DNA, clone pBUD5.
Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning and sequencing of Haemophilus influenzae outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson, M.B., Apicella, M.A., Murphy, T.F., Vankeulen, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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QQRYNTVYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALG
QRRADAVKGYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY"
                                                                                                                                                                                                                                                               /product="outer membrane protein P6'
168 c 175 g 271 t
                                                                                                                                                                                                                                                                                                                           /note="outer membrane protein P6 signal peptide"
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/protein_id="AAA24994.1"
/db_xref="GI:148961"
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BCT 29-MAY-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 867)
Murphy, T.F. and Apicella, M.A.
Plasmid for production of membrane protein, bacterium containing
same, monoclonal antibody therefore, and method for the
identification of haemophilus influenzae
Patent: EP 0281673-A1 1.14-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1 from Patent EP 0281673. I05561
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           GGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA
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Haemophilus influenzae Rd section 37 of 163 of the complete genome.
U32722 L42023
                                                                                                                                                                                                                                                                                                                 Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the corresponding H. influenzae genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae whole-genome comparison with Escherichia coli Curr. Biol. 6 (3), 279-291 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U32722.1 GI:1573348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae
                                                                                                                                            Medical Center Dr. Rockville, MD 20850, USA
The whole genome was shifted by 588 nucleotides for a new start
on Sep 30, 1996 this sequence version replaced gi:1221050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                              Submitted (28-MAY-1998) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                       White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D., Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-SEP-1997) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White, O., Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medical Center Dr, Rockville, MD 4 (bases 1 to 13620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-JUL-1995) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenzae Rd
                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8805245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAGCGTAC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAACCTGCAGTATTAGGTCACGATGAAGCTGCATATTCTAAAAACCGTCGTGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 13620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 13620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 13620)
                                                                                                                                                                                                                                                                                                      (bases 1 to 13620)
                                           complement(61.
                                                                                                          Location/Qualifiers
1. .13620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D.
complement(61. .513)
                                                             /db_xref="taxon:
                                                                                   /organism="Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (5223), 496-512 (1995)
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Rd
                                           .513)
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                                                                 71421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20850,
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Hayes, W.S., deduced from

gene CDS

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/translation="MKLLKRLYSVFAIVLAVGSNAFAGDEVRIVIDEGVDGARPIAVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="peptidoglycan-associated outer membrane lipoprotein (pal)"
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                                                                    complement(3543. .4661)
                                                                                                                      complement(3543. .4661)
                                                                                                                                                 AQISADGKTLVMINGNNNVVKQDLTTGVSEVLSTSFLGESPSLSPNGIMIIYSSTQGL
GKVLQLVSADGRFKASLPGSDGQVKFPAWSPYLTK"
                                                                                                                                                                                                   ANGGTPTQLTSGAGNNTEPAWSPDGNSILFTSDRSGSPQVYRMDASGGSATAVGGRGS
                                                                                                                                                                                                                           VSFENKKSQLVVQDLNSGARKVVASFQGHNGAPAFSPDGSRLAFASSRDGVLNIYVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to SP:P10324 PID:1573351 SP:P10324 GB:ML8878 PID:1573351 percent identity: 100.00; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                               /product="colicin tolerance protein (tolB)"
/protein_id="AAC22040.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2218. .3501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2218. .3501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="codon recognized: AAG" complement(1733, .2194) /gene="HI0381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to PID:1685080 percent identity: identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HI0382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HI0382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1733. .2194)
/gene="HI0381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1405. .1477)
/gene="tRNA-Lys-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="tRNA-Lys-3"
complemen+'''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLENIRIVLIETSHSGNIGSAARAMKTMGLTQLCLVSPKSVDEQ
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KGKIAIVFGRERIGLTNEELLKCHYHLNIPANPDYSSLNLAMAVQLVSYELRMAFLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKLTSKGRYAVTAVLDIALNADGGPVSLADISERQHISLSYLEQ LFAKLRKDGLVKSVRGPGGGYQLGLPSEQISVGMIIAAVNENIHVTKCLGRENCKNGV ECLTHELWEDLSLRIESFLNETTLAELVNKRNVKRQSHRDFNNLLVNQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELNILNGMLSAVEKRIDLTKEDN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(566. .1291)
/gene="HI0380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(566. .1291)
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/protein_id="AAC22037.1"
/db_xref="GI:1573349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:U00096 PID:1788880 percent identity: 63.38; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAC22038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
/protein_id="AAC22038.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:000096 PID:1788881 percent identity:
54.43; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="HI0380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.96;
                                                     Query Match:
                                                                                     Best Local
                                                                                                                                           Score:
                                                                                                                                                                     Pred. No.:
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                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                           gene
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Percent Similarity:
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                                                                                                                                    Scores:
                                                    Similarity:
                                                                                                                                                                          /gene="HI0387"
6606. .8528
                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to SP:P08999 PID:1128977 GB:U00096 PID:1786957 percent identity: 53.08; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="colicin transport protein (tolq)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5871. .6281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQATLQMVAPGIAEALIATAIGLFAAIPAVMAYNRLSLRVNAIEQDYGNFIDEFTTIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MARRORKAIKSEINIVPFLDVLLVLIIFMATAPIISQSVQVEL PDSVQSQEVSNEDKVPVILEVAGIGKVAISIGGERQEGLTEEMVTQLSRQEFDKDNNT LFLVGGAKEVPYEEVIKALNILHLAGIKSVGLMTNPI" complement (5168. .5854) /gene="H10385"
                                                                                                                                                                                                                                                          ftqqtlleeqqlafyvktlaidycvaaklddllmvetevsevkgatilfeqrlmrntl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5871. .6281)
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                                                                                                                                                                                                                                                                                                                                                                       transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="HI0386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HI0386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to SP:P05828 PID:1128978 GB:U00096 PID:1651329 PID:1786958 percent identity: 68.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5168. .5854)
/gene="HI0385"
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PID:1651330 PID:1786959 percent identity: 61.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4677. .5096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:1651331 percent identity: 42.58; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                              'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4677. .5096)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAEAKAKADAEAKAATEAKRKĀDQASLDDELNGGDIGGGSASKGGNTNKGGTQGSGAA
LGSGDGGKVGDQYAGVIKKEIQRRELKDPNFAGKVCRIKIQLGRDGTILGYQKISGSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HI0384"
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68.93%
49.51%
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2044 GTTTATTTCGGTTTTGATAAATATGACATTACTGGTGAATACGTTCAAATCTTAGACGCG 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1744 TTAGCGTAC 1736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capela,D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J. Boistard,P., Becker,A., Boutry,M., Cadleu,E., Dreano,S., Gloux,S., Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sinorhizobium meliloti 1021 complete chromosome; segment 10/12
AL591791 AL591688
                                                                                                                                                                                                                                                  France, Laboratoire de Genetique et Developpement UMR6061-CNRS, Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes, France, GATC GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25, D-33615 Bielefeld, Germany, Unite de Biochimie physiologique, Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20, Universite Catholique de Louvain, Unite de Microbiologie, Faculte B-1348 Louvain-la Neuve, Belgium, Unite de Microbiologie, Faculte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sinorhizobium meliloti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO EU Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sinorhizobium meliloti strain 1021
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis of the chromosome sequence of the legume symbiont sinorhizobium meliloti strain 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pohl,T., Portetelle,D., Puehler,A., Purnelle,B., Ramsperger,U., Renard,C., Thebault,P., Vandenbol,M., Weldner,S. and Gallbert,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SME591791
                                                                                                                                                                        B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr
http://sequence.toulouse.inra.fr/meliloti.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratoire de Biologie Moleculaire des Relations plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MELILO EU Consortium:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTATTTAGCTGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1481430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAAAACCTGCAGTATTAGGTCATGATGAAGCTGCATATTCTAAAAAACCGTCGTGCAGTG 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAACGTGGTACACCAGAATACAACATCGCATTAGGCCAACGTCGTGCAGATGCAGTTAAA 1865
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                                                                                                                                                                                                                            Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6,
                                                                 /organism="Sinorhizobium meliloti"
/strain="1021"
                                          /db_xref="taxon:382"
                                                                                                                                                       ocation/Qualifiers
                                                                                                                             .340900
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/note="Product confidence : putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="Sptrembl:Q92MU3"
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/translation="MANVVILVILAVGSVLFHILSPWWWTPIASNWNYIDNTITITFW
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VWNQFVTVPQDASEVEVIGQQWLWSFRLPGABCKLGTTETTDIAPENTLGVNRDDAAG
QDDIIIEGGELHILPVGREVKMLLRSVDVLHDFYVPEFRAKMDMVPGMITYFWLTPTRT
QDDIIIEGGELHILPVGREVKMLLRSVDVLHDFYVPEFRAKMDMVPGMITYFWLTPTRT
GTFEILCAELCGVGHPQMRGTVVVDTEEDYQAMLAEQQTFSQLSASSETRAVPEKVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYPEPTIDE II TRANSMEMBRANE
/protein_id="CAC47095.1"
/db_xref="GI:15075540"
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/protein_id="CAC47094.1"
/db_xref="GI:15075539"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1457. .1513)
/note="Sm-5 OR SMC04646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by Homology
predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFPSGIATEQGTGASALFKEERECFGPAATTVAASAAQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="coxM OR SMc01982"
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/db_xref="GI:15075541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted by Homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT SM-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Product confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="small molecule metabolism; energy transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                      predicted by
                                                                                                                                                                                                                                                                                                                                                         predicted
                                                                                                                                                                                                                                                                                                                                                                                      Gene name confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                         electron transport"
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/gene="coxN OR SMc01983"
/EC_number="1.9.3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="coxN OR SMc01983"
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                                                                                                                                                                                                                                                /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                             /note="Product confidence : probable
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/function="small molecule metabolism; energy transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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                                                                                                                                                                                                                                                                               /codon_start=]
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by FrameD"
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gene

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/gene="SMc01986"
4857. .5216
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TGLYWHFVDLVWVFIFAFFYLW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFLLSDTFVFGCFLLAYMSARMSTSVPWPNPSEVFALEIGGTHMPLILIAIMTFVLIS
SSGTMAMAVNYGYRBDRRKTAALMILTALFGAAFVGMQAFEWSKLIAEGVRPWGNPWG
                                                                                                                                                                                                                                                                                                                                                           predicted by Codon_usage
predicted by FrameD"
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/db_xref="SPIREMEL5042"
/tanslation="MSIVE.99MU1"
/translation="MSIVE.99MU1"
/transl
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                                                                                                                                                                                                           /transl_table=1
                                                                                                                                                                                                                                                     /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="miscellaneous; hypothetical/partial homology"
/note="product confidence : hypothetical
Gene name confidence : hypothetical
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/db_xref="GI:15075543"
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electron transport"
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4123. .4845
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EWFEGHPEVYTVALPAREJUSDLISTHARKNIFGYRMAVMAIVIIGGLSFIVWAHHMY
VSGMNPYFGFFATTILIIAVPTAIKVYNWVLTLWRGNIHLTLDMLFALAFIVTFVNG
GLTGLEIGNVVVDPLSDTMFVVAHFHMVMGVAPIMVIFGAIYHWYPKITGRMLNEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SMc01986"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="PROBABLE CYTOCHROME-C OXIDASE PROTEIN"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 LeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro 152
1 (bases I to 10906)

1 (bases I to 10906)

1 (bases I to 10906)

1 (chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F., Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F., Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G., Gillet,W., Grant,C., Guenthner,D., Kutyavin,T., Levy,R., Li,M., McClelland,E., Palmieri,A., Raymond,C., Rouse,G., McClelland,E., Palmieri,A., Raymond,C., Rouse,G., Saenphimmachak,C., Wu,Z., Gordon,D., Eisen,J.A., Paulsen,I., Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., Biddle,P., Jung,M., Krespan,W., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 PheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGly 112
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                                                                                                                                                                                                              Agrobacterium tumefaciens str. C58 (U. Washington).
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGCTCGTCATGACGCTTGCCCTTGCTGGCTGCGCTTCGAAGAAGAAC--
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Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J. A., Paulsen, I.,
Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M.,
Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C.,
Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-SEP-2001) Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Wood, I., Kitajima, J.P., Okura, V.K., Almeida Jr., N.F., Zhou, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Nester, E.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294 (5550), 2317-2323 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumefaciens C58
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/note="Atu3709"
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REQTLNQLLVEMDGFEANEGIILIAATNRPDVLDPALLRPGRFDRQVVVPNPDLVGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDGDIYRYIEFVKRTLPRDVTLSGLRIAIDCANGAAYKVAPAALWELGAEVVTIGNEP
NGININLECGSTHPEALQKKLHEVRADIGIALDGDADRVIIVDERGEIVDGDQLMAVI
ADSWAADNTLRGGGIVATVMSNLGLERFLGDKGLTLARTKVGDRYVVEHKRNHUNNVG
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/protein_id="AAL44519.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(113. .1489)
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                                                                                          RILKVHVRNVPLAPNVDLKILARGTPGFSGADLMNLVNEAALMAARRNKRVVTMQEFE
DAKDKIMMGAERRSSAMTEAEKKLTAYHEAGHAITALKVAVADPLHKATIIPRGRALG
                                                                                                                                                                                                                                                                                          DVDSGRVRDVTVTGNRVLGTYTENGTAFQTYSPVIDDSLMERLQSKNVTIVARPESDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1654. .3600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEQSGHIVLSDYGTTGDGLVAALQVLAKVKRSGLTVSEVCRKFEPVPQLLKNVRISGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRGHHRHRVVIGKDTRLSGYMLENALVAGFTAAGLDVFLLGPIPTPAVAMLTRSLRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
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located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ftsH"
/note="Atu3710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSARSAA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:180835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain="C58"
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                                                            MVMQLPEGDRYSMSYKWMVSRLVIMMGGRVAEELTFGKENITSGASSDIEQATKLARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ftsH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5111. .6100)
/gene="Atu3712"
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GMADAVLYDAHLWIMRPFLACERQVIRDYVSSRSRHWLDDPSNENIRYERVRVRQTLP
HSPIALDDSTAVRRQMLSERTAVFLRERAQVFHAALARLADDDVNPDLPEFRHGLAAL
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/gene="Atu3711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEAYKVQQLEEQIRQLIGRIEEMSFQLLQMQETIRKAQEDNEFRFQELEGGKCASPTA
APKKKABASPVNEPATEPTDDVATIIETPQGGASVSPPPSSSASTAAPGETTICASIEL
DSKCMPVGGTLNQGANNSSGSLPGVTTGNGTRKTDPVTFAALTSEGDITQAAVGHVLS
GDYKLAEQGFQQYLQGYPKGTKAADASFWLGEAQYSQGKFNEBAKTFLNGHQTYGKSP
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IESSGQAVWDDRFLVKNGSDFPINVAAGRVGTAAQAAALFPSAPSGVVKPAMAGLPQI
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EKGYEDTRVVFYSESGFKTARKRQLSIMDQOGOFTQPENWRRVAHIIADAIYERVTG
YMSFEGQQPRVYLLQLETGQREVVGNFPGMTFSPRFSPDGQKVIMSLQQDGNANIYTM
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DLRSRTTTRLINTAAIDTAPSYSPDGQRVAFESDRGGRQQIYVMADGSGQQRVSFGFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAPEMLMKLGMSLAALDNTETACATLREVPKRYPNASKTVLSKVASEQKRLSC"
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located using Blastx/Glimmer"
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ELGLGGAGSATPGSQQDFTVNVGDRIFFDTDSTSIRADAQQTLQRQAQWLSRYPNYAI
TVEGHADERGTREYNLALGARRAAATRDFLASQGVPASRMKTISYGKEKPVAVCDDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6274. .6807)
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/note="Atu3713"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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located using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(7018. .8325)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="omp16 protein"
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located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Atu3714"
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DB:
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6423 CGTGACTTCCTGGCTTCCCAGGGCGTTCCGGCCAGCCGCATGAAGACGATCTCCTACGGC 6364
                                                                                                                                                                                6543 CGCCAGGCCCAGTGGCTGTCCCCGTTACCCCGAACTACGCTATCACCGTCGAAGGCCATGCC 6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6750 GCTGTCATCGCCATGACGCTCGCGCTTGCTCTCGCAGGCTGCGCGAACAAGAAGAAC---
                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 GlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGlyVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148
                                                                                        GACGAACGCGGTACGCGTGAATACAACCTGGCGCGCCGCGCCGTCGTGCCGCCGCAACC 6424
                                                                                                                                                                                                                         GluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThr 108
                                                                                                                                                                                                                                                                                                        LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp 88
                                                                                                                                                                                                                                                                                                                                                                                                          Ala---ProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSer 68
                                                                                                                  ASPGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
                                                                                                                                                                                                                                                                      CGCATCTTCTTCGACACCGACTCCACTTCGATCCGCGCCGACGCCCAGCAGACCCTGCAG 6544
                                                                                                                                                                                                                                                                                                                                                                      GCAACGCCGGGCTCCCAGCAGGACTTCACGGTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ATGCCGAACAGC---GCCGGTGAACTCGGCCTTGGTGGCGCTGGCTCC 6649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKGSLTTSAIVHASLLAFALVSLGSPEPLDVSQAEALPVELVPI
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STDKPSDKKPGEKKQETAKSASSKESDFNADDVAALLNKQAPSGGGAKRSTQTASLGG
KKSTGGSTLSQTEMDALRGALQKNWQIIPGMADAADVRVRVTMKLDRDGTIIGRPEIE
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QAIATTGYNERIFVRADSVAAYGVVADVMARIQAAGFKNIGLVTQQKQDN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(10027. .10746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(9510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAL44526.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="tolk protein"
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/gene="tolA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein_id="AAL44525.1"
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located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:17742137"
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262.00
55.62%
38.12%
30.43%
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Indels:
Gaps:
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AE008312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 GluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hinkle, S., Slater, S.C. and Goodner, B.

Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-AUG-2001) Bioinformatics, Cereon Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 11049)
Hinkle,G., Slater,S.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Approximately 800 bp of telomeric sequence missing from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rhizobium radiobacter C58), Disease in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
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Agrobacterium tumefaciens str. C58 (Cereon)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the chromosome and 200 bp missing from the right end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridge,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="/
136. .6
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/note="(AJ243808) YaeN protein"
                                                                                   /gene="AGR_L_2252"
1857. .3188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Agrobacterium tumefaciens str. C58 (Cereon)"
/strain="C58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MA 02139, USA
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3301. .5289
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RQVVPNPDLYGRERILKVHVBNAFLANDGFEANEGIILIAATNRPDVLDFALLRACHAR
RDVPNPDRACHAR
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PASGLSEASRLARYRLIADVAREIGADLVVSGTFTVAMRAARSGSDNLGLS
GMADAVLYDAHLWIMRPFLACERQVIRDYVSSRSRHWILDDPSNENIRYERVRYRGTLP
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LHKATIIPRGRALGMYMOLPEGDRYSMSYKMMYSRLVIMMGGRYAEELTFGKENITSG
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                                                                       /gene="AGR_L_2260"
8078. .9256
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IGVMISASHNPFSDNGIKLFGPDGYKLSDELEIEDLLDKDIYAQLAKPAEIGRAKR
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GEQSGHIVLSDYGTTGDGLVAALQVLAKVKRESGLTVSEVCRKFEPVPQLLKNVRISGG
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5454. .6830
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YVGGGIGGSYVKWDKLRNTSCSVNGLGCDPTTEHGGKGKWRFAYALMAGASIDVTCNL
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US-09-674-779B-2 (1-172) x AE008312 (1-11049)
                                                                           129 ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148
                                                                                                                                                                                                                                                                                                      400 CGCCAGGCCCAGTGGCTGTCCCGTTACCCGAACTACGCTATCACCGTCGAAGGCCATGCC
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520 CGTGACTTCCTGGCTTCCCAGGGCGTTCCGGCCAGCCGCATGAAGACGATCTCCTACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 CGCATCTTCGACACCGACTCCACTTCGATCCGCGCCGACGCCCAGCAGACCCTGCAG 399
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                                                                                                                                                       GACGAACGCGGTACGCGTGAATACAACCTGGCGCTCGGCGCCCGTCGTGCCGCCGCAACC 519
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                                                                                                                                                                                                   AspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
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VCTPHLGASTTEAQUNAUTATTATAVALAGNITAGALVARAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 GluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 10643)
Eisen, J.A., Nelson, K.E., Paulsen, I.T., Heidelberg, J.F., Wu, M.,
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Hickey, E.K., Peterson, J.D., Durkin, A.S., Kolonay, J.L., Yang, F.,
Holt, I., Umayam, L.A., Mason, T., Brenner, M., Shea, T.P., Parksey, D.,
Nierman, W.C., Feldblyum, T.V., Hansen, C.L., Craven, M.B., Radune, D.,
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Venter, J.C., Tettelin, H., Bryant, D.A. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dodson, R.J., Debby, R., Gwinn, M.L., Nelson, W.C., Haft, D.H., Hickey, E.K., Peterson, J.D., Durkin, A.S., Kolonay, J.L., Yang, F., Holt, J. Umayam, L.A., Mason, T., Brenner, M., Shea, T.P., Parksey, D., Nierman, W.C., Feldblyum, T.V., Hansen, C.L., Craven, M.B., Radune, D., Vanathevan, J., Khouri, H., White, O., Gruber, T.M., Ketchum, K.A., Venter, J.C., Tettelin, H., Bryant, D.A. and Fraser, C.M.

The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium Proc. Natl. Acad. Sci. U.S.A. 99 (14), 9509-9514 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-APR-2002) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlorobium tepidum TLS. Chlorobium tepidum TLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eisen, J.A., Nelson, K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlorobium tepidum TLS
AE012837 AE006470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE012837.1 GI:21646572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Dr, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10643 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heidelberg, J.F.,
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3366. .3797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYKQGLSFAKIGDEANAKARYKDVLNLYPQSPEAKLAQKNLDKK"
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Best Local Similarity: Query Match:
US-09-674-779B-2 (1-172) x AE012837 (1-10643)
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                                                                                                                     No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEVIDGDDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAHKSGRVDAIKPAMDELSKVWSDAASNLYGQPGAEPQPETNGHAGGSKGGDGAVNAE
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                                                                                                                                                                                                                                                                                                                                                            /gene="CT0646"
                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="AAM71884.1"
/db_xref="GI: 21646582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="identified by match
                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                             /gene="CT0646"
                                                                                                                                                                                                                                                                                                                                                                                                 translation="MFVFSRFGLWRSLITSVIETSKDVPKRFFHFDSLCV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CT0645"
                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                5.82e-17
259.50
56.41%
35.90%
30.14%
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                                                                                                                                                                           .8250)
                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by Glimmer2; putative
                                                                    Conservative: Mismatches:
                                  Gaps:
                                                      Indels:
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                                  10643
56
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                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                      MEDLINE
                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                  PUBMED
                                                                           source
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QΥ

15 SerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSerGlnValMetValAla

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1864 GCGGCCATGATCATTTTGGCAGGCTGTTCTTCAAAAAGTGCA-----GTATCAACAGAT 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2218 CTGGTTAACCTTGGAGTAAGCGGAGGCCGTCTTTCTACCGTCAGTTACGGCGAAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2158 GGGACCGATGAGTACAACATCGCGCTTGGTGAGCGTCGTGCTGAAGCAGCCAGAATGTAT 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2098 GCCTGGATGCAGAAAAACCCTACTTCTGCCGTGATCATTGAGGGACATTGCGATGAGCGG 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1978 GTGAGTGTGGAAGATATCGGCCAAGGGGGCAAGGCCGGTTCAATTATTGGTGATATTTTC 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1918 GAAACCTCCAGAGCCGGTTATGGATCGGGAATGGGAGGCGGAACTGGAGCAGGAGCAGGA 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2278 CCGTTTGACCCCGGTCATAACGAAGAGGCTTGGGCAAAGAACAGAAGA 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 GlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 LeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArg 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D., Ermolaeva,M.D., Vamathevan,J., Bass,S., Qin,H., Dragoi,I., Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D., Nierman,W.C. and White,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae chromosome I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 11914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
Vibrio cholerae
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                                                                                                                                                                                                                                                                                                    Submitted (14-JUN-2000) The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                           Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D., Nierman,W.C., White,O., Salzberg,S.L., Smith,H.O., Colwell,R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406 (6795), 477-483 (2000)
                                                                                                                                                                                                                                                                                                                                                                           Mekalanos,J.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCGATTTCGACAGTTCGGCACTAAGCTCCGAAGCACAGGAACAACTCAATCAGAATGCC 2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGlyVal------AlaPro 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 11914)
                                                                                                                                                                                                                                                                       Center Dr, Rockville,
/note="biotype: El Tor"
                                                                                                                                   /strain="N16961"
                                                                                                                                                                                                                                       Location/Qualifiers
                            /chromosome="I"
                                                                /db_xref="taxon:666"
                                                                                                   /serotype="01"
                                                                                                                                                                          /organism="Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:9656353
                                                                                                                                                                                                                                                                                                                                                                                  Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11914 bp DNA linear BCT 31-304-20 _{
m jome~I}, section 167 of 251 of the complete
                                                                                                                                                                       cholerae"
                                                                                                                                                                                                                                                                                                                                                                                      and Fraser, C.M.
                                                                                                                                                                                                                                                                              MD 20850,
                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                  Research, 9712
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                                       SGGLWPEPNLSATDPSLRYDSLFFNKÄTDGQVDQLSSWNNPKAGGYDRESWYLAAERE AEGLYFWSPVYUDPYTRVEMITVSTPYYRNGQDRGVATVDLSLESLIQDYAATAEQYN LGVRUKDAFGVEVVSHRFRTYDNALVSYYSGEFINWQIEVVNANQHVDEIIFDLINL EKGLMPILLCVMVGYFLISHYWIRPIVLIAKKVSESREGEIIDIRYKSQDEIRHLID TFNQKTIYLDAEKVKAQASTKAKSAFLATLSHEIRTPMNGVLGTAQILLKDELTSKQR
                                                                                                                                                               /product="sensor histidine kinase"
/protein_id="AAF94979.1"
/db_xref="G1:9565358"
/translation="MVMAIRSSLKKKSILALTIYLAFFLAIVGTLSYWGLEVPFRKEL
/KNNLALRAELLATQIREPLNNSIGVLQSLTSJKKSAADKEEQDRALRSLFSVVGGVII
GLKFQLNSEITDGRWYYGDKARLRQIIFNLLSNAVKFTEAGFVAIGLSEESCDEENYL
                       QHLTSLYESGEHMMSLLNEILDYSKIEQGKFELDHSAFPLKSIIGSIKSIYSSLCVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPAELGHTHKKGKKEGRNRVIYSTDGKDGSR"
complement(2163, .4373)
                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                    identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                            complement(2163. .4373)
/gene="VC1831"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAF94978.1"
/db_xref="GI:9656357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2101 .2196
/gene="VC1830"
/note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2016. .2123)
/gene="VC1829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRTLSIPVNIAIAWPYGVFRDYVLRQGRKISPTGWMKNLSDLVAYVLFQSPVYAATLF
TVGASTDQIITAVATNALVSCGMGVLYGYFLDMCRRWFKVPGYTVSEG"
                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:U07069 PID:459205 SP:P54302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="VC1831"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="VC1830"
2101. .2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MWPSSAGKKLSHRAHRDVIKLPNVNLETDVLTKNA" 2101. .2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
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/db_xref="GI:9656356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2016. .2123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
/protein_id="AAF94976.1"
/db_xref="GI:9656355"
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/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1375. .1827)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKYMDIDELVACTQFKHKPLEĞLRLKPEVIEGCEQYPIPVADFKFAIIPPTTQQTIĞV
KSAEVVLPLDSSMILRHANGEQCLVRKGQSVFIPAYAEQYTIECNGRVARAFSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MYNPIQNYAWGSKTALQQLFELENPNDDDQAELWMGAHPNGCSGIAINGKIVQLSDFIAQNPNLILGEYTARQFGELPYLFKILAAFKALSIQVHPNKQQAERGFAQEEQLGIALTAAQRNYKDPNHKPELVYALTEYQAMNGFRANQEILNYFIELSIDEIQPLVNVFQSNPTEQGLRDFFSGLLSIQGEAKNRALEALMAQAKQIDLPLFQLIVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="mannose-6-phosphate isomerase"
/protein_id="AAF94975.1"
/db_xref="G1:9656354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:M15380 SP:P00946 PID:146722 GB:U00096 PID:1742663; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="VC1827"
89. .1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VC1829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="VC1828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1375. .1827)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENQYPNDIGLFAPLMLNVITLQPGEAMFLDAETPHAYLHGTGLEIMANSDNVLRAGLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MKARGPFCIRHAAADTFAMVVFCFVTGMIIEIFVSGMTFQQSLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VC1827"
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/note="similar to GB:M28232 SP:P19935 PID:148020 GB:U00096 PID:1651332; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="VCl835"
/note="similar to SP:P07176 PID:41360 PID:42257 GB:U00096
PID:1651333; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MFSNLKHVVMLMLLASAASYALAAPAPVSDLGSNVSGGSRSSEI
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VRGEMKSPSSGAGQLFTSSNDEAAQGTFSSDANEQAAYQNAVDLILKKRDYAGAIAAF
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EIVEHLDSEGKRIIWGEDRHLGAYIAKKTGADMLLWGGECVYHDEFSADALKRKKALY
DDAALLUHPESPASYVELADAVGSTSQLIKAAKTLPQKMIVATDKGIFFKMQQMVPE
KELIEAPTAGAGATCRSCAHCPWMANNGLQAIAQALKEGGKQHEIFVDEALRVKSLIP
                                                                                                                         complement(7792. .9144)
                                                                                                                                                                                             complement (7792.
                                                                                                                                                                                                                           AYAKNRRAVLVY"
                                                                                                                                                                                                                                                                                  /translation="mQLNKVLKSLLIALPVLAVTACSSSDDAANSGSQTNQSAVSTVD
SNGLNAQGQLTEQELKEQALRENQTIYFAFDNATIASDYEAMLAAHAAYLVKNPSLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(6462. .7226)
/gene="VC1834"
                                                                                                                                                           /gene="VC1836"
                                                                                                                                                                                                                                                   TIEGHADERGTPEYNIALGERRAQAVAKYLEALGVQAGQLSIVSYGEEKPLVLGQSEE
                                                                                                                                                                                                                                                                                                                                                                                    /product="peptidoglycan-associated lipoprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7242. .7760)
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GFECHSVMDGVQAITALQESSFDLVLMDNHMPLKDGIQATREIRQLPLPQAKILLFGC
TADVFKDTRDKMLSAGADDIIAKPIAEHELDMALEQHSERLYQFHREPSLPSVE"
                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:9656362"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5227. .6288)
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Best Local Similarity:
Query Match:
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                                                                                                   SOURCE
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                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                   PMU271673
                                                                                                                          KEYWORDS
                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7760 ATGCAACTTAACAAAGTTCTTAAGAGTCTGCTGATTGCGCTACCAGTTTTAGCT---GTT 7704
                                                                                                                                                                                                                                                                                                                            7295 GGTCAATCAGAAGAAGCGTACGCGAAAAACCGTCGTGCAGTTCTGGTTTAC 7245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7475 AAAAACCCCAAGCCTACGCGTAACTATCGAAGGTCACGCTGATGAGCGCGGGTACTCCTGAG 7416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7643 GTGTCTACTGTTGACTCAAATGGTCTGAATGCACAAGGTCAACTG------ACT 7596
                                                                                                                                                                                                                                                                                                                                                                             156 GlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
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                                                                                                                                                  AJ271673
AJ271673.1 GI:6977945
                                                                           Pasteurella multocida
                                                                                                                          omp 16 gene; OMP 16 protein
                                                                                                                                                                                                    Pasteurella multocida partial omp
                            Pasteurella
                                                 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                Pasteurella multocida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAsp 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCGCTTGTAGCTCAAGTGATGATGCTGCGAACTCAGGTTCTCAAACTAACCAATCAGCA 7644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGCAACTATCGCGAGCGACTACGAAGCAATGCTAGCTGCACACGCTGCTTACCTAGTG 7476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThr 95
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(bases 1 to 393)
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YQVNLSGGETKRLTWGGSQNLGGQTFGYGKFLYWNRSDSGFNAKKODLFSANGET
YQVNLSGGETKRLTWGGSQNLGGGTFGYNTATT
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                                                                                                                                             322
                                                                                                                                                                         150 GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu
                                                                                                             170 LeuSerTyr 172
                                                                               382
                                                                                                                                                                                                                                                                                                                                                                    90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                 70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-FEB-2000) Goswami P.P., National Biotechnology Centre, Indian Veterinary Research Institute, Izatnagar, Uttar
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Pasteurella multocida outer membrane protein gene,
                PMU16849
                                                                                                                                                                                                                                        GAACGCGGTACACCAGAATATAACATCGCATTAGGTCAACGTCGTGCAGATGCAGTAAAA
                                                                                                                                                                                                                                                                                              GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
                                                                                                                                                                                                                                                                                                                                                                                                    GTGTATTTCGGCTTCGATAAATACAATATCGAAGGTGAATATGTACAAATTTTAGATGCA 141
                                                                                                                                           CATTATTTATCAGCGAAAGGTGTACAAGCTGGTCAAGTATCAACAGTTTCTTACGGTGAA
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/protein_id="CAB75338.1"
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/db_xref="GI:6977946"
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LDAHAAFLNATPATKVVVEGNTDERGTPEYNIALGQRRADAVKHYLSAKGVQAGQVST
VSYGEEKPAVLGHDEAAYSKNRRAVLAY"
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/transl_table=11
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/db_xref="taxon:747"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-NOV-1994) Rickie W. Kasten, Vet. Med. PMI, University of California, Davis, CA 95616, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U16849
U16849.1
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                                                             GAGAAACCTGCTGTGTTAGGTCACGATGAAGCAGCTTACTCTAAAAACCGTCGTGCTGTG 441
                                                                                                                                      CATTATTTATCAGCGAAAGGTGTACAAGCTGGTCAAGTATCAACAGTTTCTTACGGTGAA
                                                                                                                                                                       AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                                                                                                                                                                                                                         {\tt GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp}
                                                                                              GluargProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                             GAACGCGGTACACCAGAATATAACATCGCATTAGGTCAACGTCGTGCAGATGCAGTAAAA
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YNTVYFGFDKYNIEGEYVQILDAHAAFLNATPATKVVVEGNTDERGTPEYNIALGQRR
ADAVKHYLSAKGVQAGQVSTVSYGEEKPAVLGHDEAAYSKNRRAVLAY"
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/protein_id="AAA79373.1"
/db_xref="GI:841126"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55108, USA
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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complement(1702. .2229)
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                                                                     RCKLAECRTYLQQSACHSGGWVDLLDDQEYIISDLSFHWLMGKPALEIYLKGYLKKQP
                                                                                      /translation="MLFRGYTVLSLMISLSLSSLLLLVAIAFYVDVQRONRAIHFQMQLQAELERVIQLMGKDIRRAGFRAPPETTNKVNFSLFESETQASLQLFSIHGGNVSDCILFFYVDLDMNGCLGGKFKEKTCIKDGRNNTSHLERELFGYRLNNGMLETRLTYKSAVNS
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QALNIGKLAYFIQREYRGLFSHQFSVQHAPYFYWFDTKQTSWTLTQNIEAIIIAEGDL
HIHGKGKIKGTIVTGGRLTLEPSVQVSYHKATVAYWVTQLRDWQLAEKSWHDFLL"
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/gene="pM0963"
/codon_start=1
                                                                                                                                              /product="unknown"
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/db_xref="GI:12721289"
                                                                                                                                                                                                                                                              complement (985.
                                                                                                                                                                                                                                                                                /gene="PM0964"
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                   /gene="PM0965"
                                                       HFQYETTMVAPLLNHGEKQ"
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/codon_start=1
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/db_xref="GI:12721288"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11061 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .357)
                                                                                                                                                                                                                                                                .1698)
                                       .2229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multocida"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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258.00
66.99%
48.54%
29.97%
                                                                                                                                                                                                      Mismatches:
                                                                                                                                                        Gaps:
                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                Conservative:
                                                                                                                                                                                                                                                          Matches:
                                                                                                                                                        11061
50
19
34
0
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gene

gene

SUMMARIES

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Command line parameters:

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-DB-N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=100 -OCCALICN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09674779_@CGN_1_1_208 @runat_06072003 121613_9795 -NCPU=6 -ICPU-3
-NC_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_101002:*
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2: /SIDS2/gcgdata/c
3: /SIDS2/gcgdata/c
4: /SIDS2/gcgdata/c
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6: /SIDS2/gcgdata/c
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length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xgapop 10.0 , ;
Ygapop 10.0 , ;
Fgapop 6.0 , ;
Delop 6.0 , ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   July 6, 2003, 12:16:20 ; Search time 215 Seconds (without alignments) 1801.599 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-674-779B-2
861
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Ygapext
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## ALIGNMENTS

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M. catarrhalis BASB019 protein coding sequence #1. 01-MAR-2000 (first entry) AAZ40351 standard; DNA; 519

BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy; ss.

Moraxella catarrhalis.

W09957277-A2

03-MAY-1999; 99WO-EP03038.

06-MAY-1998; 98GB-0009683.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

WPI; 2000-062148/05 P-PSDB; AAY55089.

Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections

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CC screening of genetic mutations, serotype, organism or strain components of arrays which are useful for diagnostic and prognostic components of arrays which are useful for diagnostic and prognostic cupurposes. The polypeptides can be used to produce antibodies, and as a cc target for the screening of antimicrobial drugs. The polypeptides can cc antso be used in vaccine formulations, and to identify agonists and can be used for the treatment and prevention of cd iseases including bacterial infection, otitis media in infants and continuation. The polypeptides can accumulation in the elderly, sinusitis, nosocomial infections and communiation in the middle ear, auditive nerve damage, delayed speech car of entaring, infections of the upper respiratory tract and middle ear communing, infections on some of the upper respiratory tract and middle ear communing, infections on wounds, and to thus prevent insections on wounds, and to thus prevent tissue damage and/or block the cormal progression of pathogenesis in infections initiated other than by the implantation of in-welling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, can did it is no longer common to isolate M. catarrhalis strains that are resistant bacteria. This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for for Of.

Sequence 519 BP; 139 A; 108 c; 122 G; 150 Ŧ; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large compositions. M. catarrhalis (Branhamella catarrhalis) is a large alrowed for a following the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis and analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 369-391; 545pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
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                                                                               ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly
TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys
                                              ACAGGCTGTGCCAATAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAGGT
                                                                                                                                                      ATGATGTTACATATTCAAATTGCCGCCGCCGCCGCCGCTTTATCGGTACTAACTTTTATG
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RESULT 3
This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, scrotype, organism or strain identification identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; unner respiratory tract infection; middle ear infection; therapy; ss.
                                                                                                                                                                                                       Novel BASB019 polynucleotides and polypeptides from moraxella catarrhalis used to prepare vaccines against bacterial infect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. catarrhalis BASB019 protein coding sequence #2.
                                                                                                                                                                          Claim 10;
                                                                                                                                                                                                                                                                  P-PSDB;
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                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  target for the screening of antimicrobial drugs. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists (which are bacteristatic) are used for the treatment and prevention of diseases including bacterial infection, otitis media in infants and children, pneumonia in the elderly, sinusitis, nosocomial infections and
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AAZ40353 standard; DNA; 519

US-09-674-779B-2 (1-172) x AAZ40353 (1-519)

Query Match:

Percent Similarity: Best Local Similarity:

1.68e-94 850.00 98.84% 98.26% 98.72%

Indels: Mismatches: Conservative: Matches:

0021

No.:

Sequence 519

BP;

140 A;

108 c; 120

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Η, 0

519 169

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cc identification, identification of mutation in BASBOI3 sequences, and as components of arrays which are useful for diagnostic and prognostic cc components of arrays which are useful for diagnostic and prognostic cc purposes. The polypeptides can be used to produce antibodies, and as a cc target for the screening of antimicrobial drugs. The polypeptides and cc also be used in vaccine formulations, and to identify agonists and cc antagonists. The polypeptides, antibodies, agonists and cc antagonists. The polypeptides, antibodies, agonists and antagonists and cc diseases including bacterial infection, otitis media in infants and conhidren, pneumonia in the elderly, sinusitis, nosocomial infections and conhidren, pneumonia in the elderly, sinusitis, nosocomial infections and conhidren, pneumonia in the elderly, sinusitis, nosocomial infections and conhidren, pneumonia in the elderly, sinusitis, nosocomial infections and conhidren, pneumonia in the elderly, sinusitis, nosocomial infections and conhidrent ear and middle ear also used in the prevention of of alayed speech confection. They are also used in the prevention of adhesion of bacteria cc entaring, infection of the upper respiratory tract and middle ear proteins on wounds, and to thus prevent insections of bacteria cc entaring progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M. catarrhalis strains that are can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; noscomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for disposis of disease, staying disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
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Claim 10; Fig 2; 101pp;
                       Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infect
                                                                       WPI; 2000-062148/05.
P-PSDB; AAY55092.
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Countries of artisys which are used to produce antibodies, and as a caream for the polypeptides can be used to produce antibodies, and as a calculations and to identify agonists and calculations, and to identify agonists and calculations, and to identify agonists and calculations. The polypeptides can consider a calculation of integration of the used for the treatment and prevention of confidence permanental infection, othicis media in infants and confidence, permanental in the elderly, sinusitis, nosocomial infections and confidence permanental in the middle ear, auditive nerve damage, delayed speech carning, infection of the upper respiratory tract and middle ear communitation. They are also used in the prevention of adhesion of bacteria confidence in the prevent tissue damage and/or block the implantation of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Morazella catarrhalis infections has risen dramatically, can distinct to standard antibiotics. The BASBOID products of the invention of the invention of antibactorial controls that are screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, stagis disease, or determining response of an infectious organism to drugs polynucleotides may be used as a source for hybridisation probes, and resistant bacteria. be used screen for new antibacterial compounds that may target these of L..., staging or and

Sequence 519 BP; 137 A; 111 c; 122 ç; 149 T; 0 other;

Query Match: Percent Similarity: Best Local Similarity: No . . Scores: 9.06e-94 844.00 98.26% 98.26% 98.03% Length: Matches: Gaps: Mismatches: Conservative: Indels: 519 169 0 3

US-09-674-779B-2 (1-172) x AAZ40354 (1-519)

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AGCGTTGAGATTATCAGTTTTGGTGAAGAACGCCCTATCGCATTTGGCACAAATGAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                       purification of outer membrane protein of haemophilus influenzae
   by separation from an insoluble fraction using
detergent-contg., then detergent-free buffers.
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                                                                                                                                                                                                                                                                                                          Sequence 866 BP; 252 A; 168 C; 175
                                                                                                                                                                                                                                                                                                                                  H.influenzae.
                                                                                                                                                                                                                                                                                                                                           Method claimed produces large quantities of in raising antibodies for detection, and as
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 8; 22pp; English.
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P-PSDB; AAR07145.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1989;
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         IleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSer 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 67..525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                     2.85e-23
269.50
50.00%
34.57%
31.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane protein (OMP) of H.influenzae.
                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                            G; 271
                                                                                                                                                                                                                                                                                                            T; 0 other;
                                                                                                                                                           ---ThrPheMetThrGlyCysAlaAsn 25
                                                                                                                                                                                                                                                                                                                                             the purified OMP, a vaccine against
                                                                                                                                                                                                            866
65
29
51
43
                                                           -GlyTyrThrGlyVal 44
                                                                                                                                                                                                                                                                                                                                                             useful
                                                                                                            39
                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
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                         IJ
Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.influenzae DNA fragment containing the PBOMP-1 gene
                                                                                               Outer membrane protein epitopes of Hacthe prodn. of antibodies, in vaccines diagnosis.
                                                                                                                                                                                                                                    01-SEP-1988;
21-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ03869 standard; DNA; 737
                                                                                                                                                  WPI; 1990-115815/15.
P-PSDB; AAR05797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  outer membrane
                        Sequence 737
                                                  See
                                                                         Disclosure; Fig 10; 164pp; English.
                                                                                                                                                                                      Anilionis A,
                                                                                                                                                                                                             (PRAX-) PRAXIS BIOLOGICS IN
                                                                                                                                                                                                                                                                           31-AUG-1989;
                                                                                                                                                                                                                                                                                                  22-MAR-1990
                                                                                                                                                                                                                                                                                                                          WO9002557-A
                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                     typable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1990
                                                 also AAQ03870, R03948 and AAR03949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 IleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGln :::|||:::||| |||:::|||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 GAAGGTAATACTGATGAACGTGGTACACCAGAATACAACATCGCATTAGGACAACGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 CAAATCTTAGATGCGCACGCAGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
                                                                                                                                                                                                                                                                                                                                                                                                                                      H influenzae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTATCTTACGGTGAAGAAAAACCTGCAGTATTAGGTCACGATGAAGCTGCATATTCTAAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIle 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \verb|AlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuVal| \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt LysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAla}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCGTCGTGCAGTGTTAGCGTAC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnArgArgAlaGluLeuSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGATGCAGTTAAAGGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACA 441
                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                      Seid RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins; PBOMP-1;
                                                                                                                                                                                                                                       88US-0239572
89US-0396572
                                                                                                                                                                                                                                                                           89WO-US03779
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 241..702
                                                                                                                                                                                                                                                                                                                                                 /product=PBOMP-1, outer membrane protein of H.influenzae
                           225
                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GTTGCTGATCTTCAACAACGTTACAACACC---
                           A; 134 C; 154 G; 224 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                     non-typable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTT
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                                                                                                                                                                                        Deich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                        RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                      active immunisation;
H influenzae; ss.
                                                                                                            Haemophilus influenzae- used in nes and for prodn. of reagents for
                                                                                                                                                                                        Zlotnick GW,
                            0
                            other;
                                                                                                                                                                                          Green BA;
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RESULT 8
AAN81194
ID AAN8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match: DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                         CDS
Disclosure; ; pp; English
                    Plasmids, E.coli, hybridomas and for use as vaccine and detection
                                                                                 Murphy TF, Apicella MA;
                                                                                                     (UYNY-) RES UNIV NEW YORK
                                                                                                                          08-OCT-1987;
08-NOV-1986;
                                                                                                                                                        12-NOV-1987;
                                                                                                                                                                            14-SEP-1988
                                                                                                                                                                                                 EP281673-A.
                                                                                                                                                                                                                                                                       Haemophilus
                                                                                                                                                                                                                                                                                          pneumonia; meningitis;
                                                                                                                                                                                                                                                                                                    Haemophilus influenzae; 16600
                                                                                                                                                                                                                                                                                                                    16600 dalton outer membrane protein of non-typable H influenzae
                                                                                                                                                                                                                                                                                                                                              10-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                    AAN81194;
                                                                                                                                                                                                                                                                                                                                                                                     AAN81194 standard; DNA; 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                             1988-258472/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 CACGCTGCATATTTAAATGCAACACCAGCTGCTAAAGTATTAGTAGAAGGTAACACTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 GTTTATTTCGGTTTTGATAAATATGACATTACTGGTGAATACGTTCAAATCTTAGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
                                                     AAP80593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTTATTTAGCTGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                              TTAGCGTAC 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAAAACCTGCAGTATTAGGTCATGATGAAGCTGCATATTCTAAAAAACCGTCGTGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACGTGGTACACCAGAATACAACATCGCATTAGGCCAACGTCGTGCAGATGCAGTTAAA
                                                                                                                                                                                                                                                                      influenzae.
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                       87US-0092948
86US-0932872
                                                                                                                                                       87EP-0116699
                                                                                                                                                                                                                                       68..530
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                   /product=16600 dalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.07e-22
264.00
68.93%
49.51%
30.66%
                                                                                                                                                                                                                                                                                                                                                                                                                                                   172
                                                                                                                                                                                                                                                                                           SS
                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                               dalton outer membrane protein (OMP);
                   antibodies from H.influenzae protein of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative: Mismatches: Indels:
                  Haemophilus
                                                                                                                                                                                                                    OME
                 influenzae
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51
20
32
0
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RESULT 9
AAQ45440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
 18-NOV-1986;
08-OCT-1987;
                                                                                                                                                                                                                                identification; pneumonia; bacteraemia; meningitis;
postpartum sepsis; acute febrile tracheobronchitis;
                                                                                                                                                                                                                                            Outer membrane protein; vaccine; antibody; treatment; detection; identification; pneumonia; bacteraemia; meningitis;
                                           18-NOV-1986;
                                                                    05-APR-1994.
                                                                                                US5300632-A
                                                                                                                                                                                          Haemophilus influenzae.
                                                                                                                                                                                                                                                                                     Fragment encoding outer membrane protein P6 of H. influenzae.
                                                                                                                                                                                                                                                                                                                   18-OCT-1994
                                                                                                                                                                                                                                                                                                                                              AAQ45440;
                                                                                                                                                                                                                                                                                                                                                                       AAQ45440 standard; DNA; 1019 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An epitope of the protein encoded by this sequence is recognised by the 7F3 antibody in a number of isolates. Monoclonal antibodies to the 16600 D OMP are produced by hybridomas and used to detect H.influenzae. A suspect sample is contacted with the MAb in the presence of an indicator such as radiolabelled probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 867 BP; 253 A; 169 C; 174 G; 271 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                                                                                               518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150
                                                                                                                                                                                                                    otitis media; Haemophilus influenzae; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTTCAAATCTTAGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACGCAGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTAGAAGGTAATACTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAAACCTGCAGTATTAGGTCACGATGAAGCTGCATATTCTAAAAACCGTCGTGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACGTGGTACACCAGAATACAACATCGCATTAGGACAACGTCGTGCAGATGCAGTTAAA
                                                                                                                                                                                                                                                                                                                (first entry)
87US-0092948
               86US-0932872
                                         86US-0932872
                                                                                                                    /*tag= a
/product= P6 outer membrane protein
                                                                                                                                      /*tag=
                                                                                                                                                   220..68
                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.34e-22
264.00
68.93$
49.51$
30.66$
                                                                                                                                                                                                                                                                                                                                                                                                                             526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    867
51
20
32
0
                                                                                                                                                                                                                              neonatal sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
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RESULT 10
AAT42063/C
ID AAT420
XX AAT420
XX AAT420
XX AAT420
XX AAT420
XX Genome
KW Genome
KW organi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzas and so antibodies to the OMP can be used to identify H. influenzas in clinical samples. The OMP can also be used in the development of vaccines against H. influenzas which causes pneumonia, bacteraemia, meningitis, postpartum sepsis and acute febrile tracheobronchitis in adults and neonatal sepsis ancacute ofitis media in infants and children.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purifying outer membrane protein of Haemophilus influenzae extn. with detergent buffer, treatment with RNase and solubilising by heat-treating in detergent-free buffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1989;
12-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-109467/13.
P-PSDB; AAR51161.
Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1019 BP; 310 A; 200 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Column 21-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                              AAT42063 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The P6 outer membrane protein (OMP) is conserved among strains of
                                                                  Haemophilus influenzae complete genome sequence.
                                                                                                   14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No . :
                                                                                                                                                                                                                                                                                                                                                                                                                   490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 CACGCAGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTAGAAGGTAATACTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
                                                                                                                                                                                                                             TTAGCGTAC
                                                                                                                                                                                                                                                         LeuSerTyr 172
                                                                                                                                                                                                                                                                                         GAAAAACCTGCAGTATTAGGTCACGATGAAGCTGCATATTCTAAAAAACCGTCGTGCAGTG
                                                                                                                                                                                                                                                                                                                   GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                        AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu
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Matches:
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21-APR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae Rd genome medium - useful for identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments by homology searching
                                                                                                                                                            401840 GTTTATTTCGGTTTTGATAAATATGACATTACTGGTGAATACGTTCAAATCTTAGACGCG
                                                                                                401660 GGTTATTTAGCTGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA
                                                                                                                                                                                                                           401780 CACGCTGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTAGAAGGTAACACTGAT
   170 LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                    70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
                                                                                                                                                                                                                                                         90 \verb| GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 77.2-77.1091; 1291pp; English.
                                 GAAAAACCTGCAGTATTAGGTCATGATGAAGCTGCATATTCTAAAAACCGTCGTGCAGTG
                                                               GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu
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95US-0426787.
95US-0476102.
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Conservative:
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                                                                                                                                                                                                                                                                                                  A pure antigenic peptide or protein related to an epitope of Haemophilus influenzae is claimed. Also claimed is a recombinant vector comprising a DNA sequence coding for an antigenic determinant of an Haemophilus influenzae outer membrane protein, the transformed cell, a subunit vaccine in a pharmaceutical carrier, a method of immunising humans and an assay for Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                      used
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                                                                                                                                                                                                                                                                                 Sequence 737 BP; 225 A; 133 C; 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-DEC-1986;
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02-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                               peptide related to epitope of Haemophilus influenzae - as immunogens in vaccines and for producing antibodies for
                     110 GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                391 GTTTATTTGGGTTTTGATAAATATGACATTACTGGTGAATACGTTCAAATCTTAGATGCG 450
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GAACGTGGTACACCAGAATACAACATCGCATTAGGCCAACGTCGTGCAGATGCAGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP80665
                                                                                                                                                                                                                                                                                                                                                                                                                     immunisation and assays
                                                CACGCTGCATATTTAAATGCAACACCAGCTGCTAAAGTATTAGTAGAAGGTAACACTGAT
                                                                     GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                    ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluIIIIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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86US-0948364.
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CC This sequence encodes a H. pylori outer membrane protein.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC isolated from H. pylori by pCR amplification for recombinant polypeptide
CC Note: This DNA sequence is not reproduced in the specification and
CC has been derived from the related specification, W09719098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and polypeptide(s) - useful for vaccines to treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Berglindh OT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                      infection, and to detect Helicobacter
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                                                                                                                                                                                                                                                                       H. pylori outer membrane protein ORF 31262.aa
                                                                                                                                                                                                                                                                                                                                               AAT77469;
                                                                                                                                                                                                                                                                                                                                                                             AAT77469 standard;
                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                                                                                                                                            11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match:
                 29-MAY-1997
                                                    WO9719098-A1
                                                                                                                                                      Helicobacter pylori.
                                                                                                                                                                                         detection; antisense;
                                                                                                                                                                                                       activator;
                                                                                                                                                                                                                         secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No . :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACCAGCTCCAGAGAAAGAAGAGCCTAAACAAGAGCCAGCTCCAGTGGTTGAAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAGACTGTGGCTGGCGATGTGAGCACTAAAGCGGTTCAGACTGCGCCTGTTACTACA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGTATTTAGTTTCTTGGTAGCTTTTTTATTGGTAGTTGGCTGTAGTCATAAAATGGAT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerValLeuThrPheMet---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAGAAAAAGATATGATCAAAAACCATCAGTTTTTGGCGAAAAGCAAACCCAAATGCGTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAAAACGCTTTAGTCATTAAAGGG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCAC---ATGCAAGTGCTTTTGGAAGGCAATACCGATGAATTTGGCTCTAGCGAATAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGAGATCAAAGAATCCGATCAAGAGACTTTAGATGAGATCGTGCAAAAAGCTAAAGAA 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAACTAGAGAATGTTACAGAGAAAACAGAAGAGTGGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly
                                                                                                                                                                                                    rane; cytoplasmic; cell envelope; flagella; transport;
periplasmic; chronic gastritis; duodenal ulcer disease;
; inhibitor; bacterial life cycle; vaccine; immunise;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽₽;
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                                                                                                                    Location/Qualifiers
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215.50
50.00%
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25.03%
                                                                                                        .540
                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                         inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc are used to evaluate compounds, especially activators or inhibitors of compounds. The nucleic acid compounds and the pylori nucleic acid compounds are compounded and the proteins, are compounded and the proteins of a sequences. The subjects against H. compounds of the presence of these sequences in compound to inhibit expression of a gene from Helicobacter species. H. compounds the presence of these sequences are compounded to inhibit expression of a gene from Helicobacter species. H. compounds the provided and nebulised to a median size of complementary to the BstXI-cut pMPX vectors, while the overhang is not complementary. Therefore the linkers will not concatemerise nor complementary. Therefore the linkers will not concatemerise nor complementary. Therefore the linkers will not concatemerise nor complementary to the Double of the sily. The linker adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                         QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes an H. pylori outer membrane protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 108; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 540 BP; 190 A; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequenced
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                                                                                                                                                                                                              133
                                                                                                                                           193
        307
                                                                        247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The ORF/protein reference number for this sequence was obtained the related specification, W09640893.
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       AACCAC---ATGCAAGTGCTTTTGGAAGGCAATACCGATGAATTTGGCTCTAGCGAATAC
                                                                                                                                                                                                           GAACCAGCTCCAGAGAAAGAAGAGCCTAAACAAGAGCCCAGCTCCAGTGGTTGAAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                  SerValLeuThrPheMet-----
                                                                          TATGAGATCAAAGAATCCGATCAAGAGACTTTAGATGAGATCGTGCAAAAAGCTAAAGAA
                                                                                               AspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThr
                                                                                                                                           CCGGCTATTGAA-----
                                                                                                                                                                                                                                            \verb|AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp|
                                                                                                                                                                                                                                                                                                                                                   TCTGTATTTAGTTTCTTGGTAGCTTTTTTATTGGTAGTTGGCTGTAGTCATAAAATGGAT
                               AsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyr 116
                                                                                                                                                                         {\tt GluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSer}
                                                                                                                                                                                                                                                                               AATAAGACTGTGGCTGGCGATGTGAGCACTAAAGCGGTTCAGACTGCGCCTGTTACTACA 132
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Matches:
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Indels:
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This invention describes a novel preparation of an agent (A) for CC detection, prevention and/or treatment of microbial infection by: (i) identifying essential genes (I) and corresponding polypeptides (II); (ii) identifying compounds that are directed against (II) and CC inactivate the microbe; (iii) testing these for suitability for use; and CC (iv) formulating selected (A). Identifying essential genes (I) comprises (IV) formulating selected (A). Identifying essential genes (I) comprises (IV) perparation of gene-deficient microorganisms by conditional antisense (IV) formulating viability and/or survival of the deficient organisms. (IV) for products of the invention have antibacterial activity. (A) (which may be a nucleic acid (Ia), vector or host cell containing (Ia), derived (II) polypeptide (IIa), or fragments, (IIa) reparticularly used for diagnosis, (IIa) and (IIa) are used in DNA, subunit or live vaccines. The method (IIa) and (IIa) genes including those that have homology in other (III) specific antibody in other (III) can be screened quickly, in an automated process, and the intertifical can be screened quickly in an automated process, and the intertifical can be screened quickly in an automated process, and the intertifical can be screened quickly in an automated process.
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17-JUN-1999;
21-JUL-1999;
   Sequence 540 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification o
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 37; Page 252-253; 366pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                           essential genes in defective mutants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apfel H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN (CREA-) CREATOGEN GMBH.
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                            ficient cells can be screened quickly, in an automated process, identified genes can be used for screening without purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB46316
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99DE-1027740.
99DE-1034029.
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125 G; 134 T; 0 other;
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                             19-DEC-1996.
                                                                                                                                                                                               Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
                                                        WO9640893-A1
                                                                                                                                                       Helicobacter pylori.
                                                                                                                                                                                                                                            H. pylori outer membrane protein ORF 07gp31516orf4.
                                                                                                                                                                                                                                                                             21-JUL-1997
                                                                                                                                                                                  duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
                                                                                                                                                                                                                                                                                                                                    AAT68048 standard;
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No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 IleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 AATAAGACTGTGGCCGGCGATGTGAGTGCTAAAACGGTTCAGACTGCACCTGTTACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                ThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACCAC---ATGCAAGTGCTTTTGGAAGGCAATACCGATGAATTTTGGCTCTAGCGAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerGlnValMetValAlaPro---AsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
                                                                                                                                                                                                                                                                                                                                                                                           AAAACTAGAGAGTGTTATAAAGAAAACAGAAGAGTGGATGTC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAGAAAAAGATATGATCAAAACCATCAGTTTTGGTGAAACCAAAACCCAAATGCGCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCAAGCGCTTGGCGTTAAAAAGGACTTTGAGCGTGAAAAACGCTTTAGTCATTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyr
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                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.83e-17
215.50
51.72%
32.18%
25.03%
                                                                               "no stop codon given"
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06-JUN-1996;

96WO-US09122

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Query Match:
DB:
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The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or previnfection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 561 BP;
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                                                                                                                                                                                                                                                                                                                      GAACCAGCTCCAGAGAAAGAAGAGCCTAAACAAGAGCCAGCTCCAGTGGTTGAAGAAAAG 216
                                                                                                                                                                                                                                                                                                                                                     AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp 56
                                                                                                                                                                                                                                                                                                                                                                                        AATAAGACTGTGGCTGGCGATGTGAGCACTAAAGCGGTTCAGACTGCGCCCTGTTACTACA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGTATTTAGTTTCTTGGTAGCTTTTTTATTGGTAGTTGGCTGTAGTCATAAAATGGAT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerValLeuThrPheMet-----
IleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly 156
                                                                  AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGly 136
                                                                                                        AACCAC---ATGCAAGTGCTTTTGGAAGGCAATACCGATGAATTTGGCTCTAGCGAATAC 387
                                                                                                                                       AsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyr 116
                                                                                                                                                                            TATGAGATCAAAGAATCCGATCAAGAGACTTTAGATGAGATCGTGCAAAAAAGCTAAAGAA 330
                                                                                                                                                                                                                                                  CCGGCTATTGAA-----AGCGGGACTATCATCGCTTCTATTTATTTTGATTTTGACAAG 270
                                                                                                                                                                                                                                                                                 GluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSer 76
                                      AACCAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAAAACGCTTTAGTCATTAAAGGG 447
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95US-0487032
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215.50
50.00%
32.76%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ThrGlyCysAlaAsnLys-----
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RESULT 16
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                                                                                                  US-09-674-779B-2 (1-172) x AAV90653 (1-770)
                                                                                                                                              Query Match:
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                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                            antibody-detection assays, on sera, plasma, urine, saliva etc., they highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antig are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV90653 standard; DNA; 770
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peptic ulcer;
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                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chow TP,
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25-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Page 143-144; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1998;
                                                                                                                                                                                                                                                   Sequence 770 BP; 264 A; 132 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     long-lasting immune response
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                                                                                                                                                                                                          No.:
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ThrSerGlnValMetValAlaPro---AsnAlaProThrGlyTyrThrGlyValIleTyr 46 ::::::: :::
                                            AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fry KE,
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97US-0045107
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                                                                                                                                2.95e-16
211.50
52.02%
31.21%
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20
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                                                                                                                                   Gaps:
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gastric lymphoma; ss.
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54
36
72
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RESULT 17
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  antibody-detection assays, on sera, plasma, urine, saliva etc., highly sensitive and specific. The specification also describes previously unrecognised immunogenic cluster families. H. pylori
                                                                          The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In
                                                                                                                                                                                                                                                                                   New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                Claim 20; Page 281; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; immunogenic cluster family; vaccine; peptic ulcer; gastric adenocarcinoma; gastric
                                                                                                                                                                                                                                                                   long-lasting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENELABS TECHNOLOGIES
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25-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Fry KE,
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97US-0045107
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lymphoma; ;
H. pylori
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antigens
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27-APR-1998;
                         05-NOV-1998
                                                  W09849314-A2
                                                                                                                                         Nucleotide sequence from clone
                                                                                                    Antigen; immu
peptic ulcer;
                                                                                                                                                                                            AAV90545;
                                                                                                                                                                                                                      AAV90545 standard;
                                                                         Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
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                                                                                                   immunogenic cluster
lcer; gastric adenoca
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                                                                                                                                                                 (first entry)
98WO-US08487
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211.50
52.02%
31.21%
24.56%
                                                                                                                                                                                                                      DNA;
                                                                                                   adenocarcinoma;
                                                                                                                                                                                                                      1610
                                                                                                               family;
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Matches:
Conservative:
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Indels:
                                                                                                             vaccine;
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                                                                                                gastritis;
lymphoma; s
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11
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653

536

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137 713 157 416

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
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25-APR-1997;
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                                 1460 GAAAAAGATATGATCAAAACCATCAGTTTTGGTGAAACCAAACCCAAATGCGCCCAAAAA 1519
                                                                                                                                                                     1343 CAC---ATGCAAGTGCTTTTGGAAGCCAATACCGATGAATTTGGCTCTAGCGAATACAAC
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                                                                                                                                                                                                                                                                       GluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsn 97
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AsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                  AsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThr
                                                                                                      CAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAAAACGCTTTAGTCATTAAAGGGGTA 1459
                                                                                                                                  MetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIle 137
                                                                                                                                                                                                                                        GAGATCAAAGAATCCGATCAAGAGACTTTAGATGAGATCGTGCAAAAAGCTAAAGAAAAC
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97US-0045107.
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DB:
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                                                      Percent Similarity:
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                                                                                                                                       Sequence 435 BP;
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AAT74194 standard; DNA; 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omp22 gene; outer membrane protein; antigen; immunogen; stomach; gastritis; peptic ulcers; gastric cancer; diagnostic; vaccine; d
                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori outer membrane protein, Omp22 - used in vaccine for treatment or prevention of H. pylori infection
                                                                                                                                                                                                     ingredient in a diagnostic kit or a vaccine
                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Pages 20-22; 38pp; English.
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7.19e-16
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38.02%
23.87%
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21-JUL-2000;
07-AUG-2000;
18-AUG-2000;
14-SEP-2000;
                                                                                        03-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carctid artery stenosis; myocardial infarce cerebrovascular disease; aortic aneurysm; claudication; stroke;
                                                                                                                 03-JUL-2001;
                                                                                                                                                                  WO200202606-A2
                                                                                                                                                                                                                 mat_peptide
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   10-NOV-2000;
22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                       CWL029; open reading frame; ORF; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAAACCCAAATGCACCCAAAAAACTAGAGAGTGTTATAAAGAAAAACAGAAGAGTGGAT
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                                                                                                                                                                                                                                                                                                                   pneumoniae
2000GB-0016363.
2000GB-0017047.
2000GB-0017983.
2000GB-0019368.
2000GB-0020440.
2000GB-0022583.
2000GB-0027549.
2000GB-0031706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          them. The proteins are predicted to be immunogenic and may therefore be cuseful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is calso involved in the development of cardiovascular diseases such as composed in the development of cardiovascular diseases such as composed in farction, cerebrovascular disease, carotid artery stenosis, composed in receivable of the invention claudication and stroke. The proteins and nucleic acids of the invention composed in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of chamydia probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a compositically claimed DNA which encodes a Chlamydia pneumoniae protein of the invention.
AAD08593 standard; DNA; 779 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Chlamydia pneumoniae protein useful in the manufacture medicament for treatment or prevention of infection due to CP preferably Chlamydia pneumoniae, and for diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 579 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
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                                                                     502 CATCCTTTAAATTCGGGACACAACGAACTAGCATGGCAACAAAATCGCCGTACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                             PheAspPheAspSerAspGluIleLys---ProGlnAlaAlaIleLeuAspGluGln
                                                                                                     ArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                          TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu
                                                                                                                                                                                                                                                 {\tt ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn}
                                                                                                                                                                                                                                                                                        GTTCACTACATGAAGAAAAACCCGAAAGCTACACTGTACATTGAAGGGCATACTGACGAG
                                                                                                                                                                                                                                                                                                                          AlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu
                                                                                                                                                                                                                                                                                                                                                               TTTGCTACAGACAGCTATACAATTAAAGGTGAAGAGAACCTTGCGATTCTCACGAACTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu-----ValTyr 71
                                                                                                                                                                                                                 CGTGGAGCTGCATCCTATAACCTTGCTTTAGGAGCACGACGAGCCAATGCGATTAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 60-61; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 A; 131 C;
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                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                          Alignment
                                                                                                                                                                                                                                                                                                                                                                                           or express it in a non-toxic, mutated form. The omp P6 probes are useful in diagnostic tests as capture or detection probes and the primers are useful in diagnostic methods involving PCR (polymerase chain reaction).
                                                                                                                                                                                                                                                                                                                                                                                                                                        of omp P6 precursor protein and their corresponding DNAs are useful in vaccine composition. The polynucleotide is useful in the construction of attenuated Chlamydia strains that can over express the polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (omp) P6 precursor gene. The omp P6 precursor polynucleotide, polypeptide and its antibody are useful for detecting, preventing and treating chlamydia infections e.g. pneumonia, upper respiratory tract diseases (e.g. bronchitis, sinusitis) and acute respiratory diseases (e.g. cough, sore throat). C. pneumoniae infection is also observed to be associated with atherosclerosis and asthma. Immunogenic fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is Chlamydia pneumoniae outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia polypeptides and polynucleotides for preventing, diagnosing and treating Chlamydia infection in mammals, especially humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩PI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murdin AD, Oomen RP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumonia; upper respiratory tract disease; bronchitis; sinusitis;
acute respiratory disease; cough; sore throat; atherosclerosis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae omp P6 precursor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                             The antibody is useful for purifying polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVET ) AVENTIS PASTEUR LTD.
                                                                                                                                                                                                                                                                                                                                           Sequence 779 BP;
                                                                                                                                                                                                                            Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P6 precursor;
                                                                                                                                                                                                                                                                                                           Scores:
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                                     362 TTTGCTACAGACAGCTATACAATTAAAGGTGAAGAACCTTGCGATTCTCACGAACTTG
                                                                                                      302 GATTCCAAAGAAAAAAACAATACAAGTCAAGCCAAGTTGCAGCATTTCGTAATATCACC
     91
                                                                     72 PheAspPheAspSerAspGluIleLys---ProGlnAlaAlaAlaIleLeuAspGluGln
                                                                                                                                   54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu-----ValTyr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 1; 74pp; English.
   AlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Omp P6 precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                           240 A; 175 C; 150 G; 214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outer membrane protein; Chlamydia infection;
respiratory tract disease; bronchitis; sinusitis;
                                                                                                                                                                                                        204.50
58.82%
38.66%
23.75%
22
                                                                                                                                                                                                                                                                                           2.14e-15
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                                                                                                       Pred.
US-09-674-779B-2 (1-172) x AAX91990 (1-1230025)
                                          Query Match:
                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                         The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX91990 standard;
                                                                                                       . No.:
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21-NOV-1997;
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                                                                                                                                                   Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589
                                                                                                                                                                              Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 291-611; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffais R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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97FR-0014673.
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                               204.50
58.82%
38.66%
23.75%
                                                                                                          6.07e-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome of Chlamydia pneumoniae
                                              Mismatches: Indels:
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Conservative:
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                                  2 3 4 6 6
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AAZO1425/c
ID AAZO14
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AC AAZO14
AX O7-OCT
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Comple
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Vaccin
KW Vaccin
KW Parattr
KW Nongon
KW Wo9928
AX Chlamy
YX
PR 10-JUN
XX
PF 27-NOV
YX
PR 17-DEC
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PF 17-DEC
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PR 17-DEC
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CC GEST
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PI Griffa
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PT Genome
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 The present sequence represents the complete genome of Chlamydia trachomatis. Open reading frames (ORFs) of the genome encode polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, peeindymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in trachoma diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                          Claim 1; Page 373-656; 1755pp; English.
                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                          WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                              Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence of Chlamydia trachomatis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bartholinitis; pneumopathy; venereal lymphogranulomatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eye disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu 150
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97FR-0015041.
97FR-0016034.
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RESULT 24
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                                      25-JUN-1999;
           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                23-JUN-2000;
                                                                                                                     WO200100836-A1
                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis DNA encoding BASB113 protein.
                                                                                                                                                                                                                                Moraxella catarrhalis
                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                        diagnosis;
                                                                                                                                                                                                                                                                              BASB311; infection; otitis media; pneumonia; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                       AAF30043;
                                                                                                                                                                                                                                                                                                                                            23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                AAF30043 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               832873 CATCCTGTTCATCCAGGCCATAATGAATTAGCTTGGCAACAAAATCGTCGTACTGAA 832817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832993 CGTGGAGCTGCAGCTTATAACCTAGCTTTAGGAGCTCGTCGTGCGAATGCTGTAAAACAA 832934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      833173 TCCAAAGAAGAGCAGCTGTACAAAACGAGCGCACAGAGTACCTCTTTCCGAAATATCACT 833114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            833233 GGATTCGTACCTTTCTACTCCGATGAAGAATTCAACAAGCTTTTGTTGAAGATTTTGAT 833174
                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 ArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 AlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
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                                                                                                                                                                                                                                                             SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheAspPheAspSerAspGluIleLysProGln---AlaAlaAlaIleLeuAspGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLeu-----
                                                                                                                                                                                                                                                                  antibacterial; antimicrobial; genetic immunisation;
                                                               2000WO-EP05851
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                   99GB-0015044.
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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196.50
48.92%
35.25%
22.82%
                                                                                                                                                         "a polynucleotide having this
                                                                                                                                            also specifically claimed in
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Claim 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of DNA encoding BASB113 protein (see AAB20105) of Moraxella catarrhalis Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The DNA was obtained from M. catarrhalis plasmid DNA by PCR amplification (see also AAF30044-45). The invention provides BASB113 polypeptides, and polynucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 expression vectors, most cells and methods for producing BASB113 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB113 polypeptide, an immunogenic fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a polypeptide are the productive comprising a polypeptide mathod of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide encoding such a polypeptide. A claimed method of diagnosing a Moraxella infection involves identifying a BASB113 polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least lantibody directed against a BASB113 polypeptide. BASB113 polynucleotides also have utility in diagnosis of the stage and type of infection, and also for therapeutic or prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 67; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB20105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 675 BP; 189 A; 124 C; 190 G; 172 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purposes, in particular genetic immunisation.
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                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 AAAACAGGTCGTGATGCCATTTTG----GGGGCGGCAGTTGGTGCAGCAGCAGGGGGCGTAT 240
133 LeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro
                                                                                                                                                                                                                                355
                                                                                                                                                                                                                                                                                                                                                                                                                 241 ATGGAGCGTCAAGCAAAGCAGATTGAGCAACAATGCAAGGAACGGGCGTGACT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46
                                             CAAGCGGCTTATAATCAAGAGCTGTCTGAGCGTCGAGCGGATTCAGTGCGTTATTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGGGGCTGTGGCAGTGCACTTGGCGGTACTGCCATTTCAAAAGCAACTGGTGGCGAA
                                                                       SerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu 132
                                                                                                                                                                                   PheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGly 112
                                                                                                                                                                                                                              GCTCATGATGACGATACTTTAAACAGTGCATTTTTGGGTCGTTTAAACCAGCTGGCTAAT 414
                                                                                                                                                                                                                                                                        AspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGln 92
                                                                                                                                                                                                                                                                                                                        GTAACCCACGATACCGACACGGGTAATATTAATCTAACTATGCCAGGTAATATTACTTTT
                                                                                                                                                                                                                                                                                                                                                                   ValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPhe 72
                                                                                                                                        ACGATGAATCAGTATCATGAAACAACGATTGTCATTGTAGGACATACAGACTCAACGGGT 474
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180.50
41.01%
26.97%
20.96%
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P 04

4099 AAAACAGGTCGTGATGCCATTTTG----GGGGCGGCAGTTGGTGCAGCAGCAGGGGGCGTAT

SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46

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RESULT 25
AAF28526
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                                                             US-09-674-779B-2 (1-172) x AAF28526 (1-31940)
                                                                                                          Query Match:
                                                                                                                            Best Local Similarity:
                                                                                                                                          Percent Similarity:
                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                             The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aldentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic library; bacteria; human upper airway; otitis media; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic fragment #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF28526 standard; DNA; 31940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200078968-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-2000; 2000WO-US16649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis.
                                                                                                                                                                                                                                                                 aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonar infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-041427/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000
                                                                                                                                                                                                                        Sequence 31940 BP;
                                                                                                                                                                                                                                                       and meningitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                             7 IleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                               Page 115-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCATCGAATGCAACCGAAGCAGGTCGTGCTCAAAATCGCCGTGTTGAGCTG
ATTGGGGCTGTGGCAGTGCACTTGGCGGTACTGCCATTTCAAAAGCAACTGGTGGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                              3.22e-10
180.50
41.01%
26.97%
20.96%
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                                                                                                                                                                                                                                                                                                                                                                                                                               545pp; English
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                                                                                              Gaps:
                                                                                                                              Mismatches:
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88
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This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify
                                                                                                                     Claim 1; Page 77.2-77.1091; 1291pp; English
                                                                                                                                                                  Haemophilus influenzae Rd genome recorded on computer readable medium - useful for identifying commercially important nucleio
                                                                                                                                                                                                                            WPI; 1996-485782/48
                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
21-APR-1995;
                                                                                                                                                         fragments by homology searching
                                                                                                                                                                                                                                                               Adams MD,
                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae complete genome sequence
                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
(UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism; open reading frame; ORF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGATGAATCAGTATCATGAAACAACGATTGTCATTGTAGGACATACAGACTCAACGGGT 4389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGln 92
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                                                                                                                                                                                                                                                           Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                            95US-0487429.
95US-0426787.
95US-0476102.
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                                                                                                                                                                                                                                                           Smith HO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation; gene expression;
                                                                                                                                                                   commercially important nucleic
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                                                                                                                                                                                                                                   P. aeruginosa OprF-OprI hybrid gene
              16-DEC-1994;
                                               17-NOV-1995;
                                                                                                                                               Pseudomonas aeruginosa serotype 6 (ATCC 33354)
                                                                                                                                                                                antibody; glutathione-S-transferase; GST; ds.
                                                                                                                                                                                                      Vaccine;
                                                                                                                                                                                                                                                                        01-OCT-1996
                                                                                                                                                                                                                                                                                                                                           AAT32600 standard;
                                                                                19-JUN-1996
                                                                                                                                                                                                                                                                                                          AAT32600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                1235692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1235335 CGTTTTGGTCAAGGCGCAGCACCAGTTGTTGCAGCACCTGAAGTTGTAAGCAAAACTTTC 1235394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1235275 CCAAATACCGCACTTAACTACAACCCTTGGATTGGTTCTATCAATGCGGGTATTTCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 AlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleTleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu------
                                                                                                                                                                                                 fusion protein; OprF; OprI;
                                                                                                                                                                                                                                                                                                                                                                                                           CGTAAAGCGCTTATCGCTTGTTTTGCTCCAGACCGTCGTGTAGAAATCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAACTGGCTACGGTAAAGCAAACCCAGTAACTGGTGCAACTTGTGACCAAGTTAAGGGT 1235691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
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              94EP-0120023
                                             95EP-0118098
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RESULT 28
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 13-14; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was expressed in Escherichia coli and Saccharomyces cerevisiae transformants. The oprF-oprI hybrid protein, and antibodies raised against it, conferred protection against P. aeruginosa infection in laboratory animals. The hybrid protein was significantly more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion
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         AAQ54144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic than an oprI-oprF fusion (AAR99627).
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                               AAQ54144 standard;
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                                                                                                                                                                                                                                                                                                                                                                                              GCTCCGACTCCGACAACGACGGCGTCTGCGACAAC-GTCGACAAGTGCCCGGACACCCCG
                                                                                                                                                                                                                                                                                                         CTGGACGTGAAGTTCGACTTCGACAAGTCCAAGGTCAAAGAGAACAGCTACGCTGACATC
                                                                                                                                                                                                                                                                                                                                                  GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                   AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
                                                                                                  ArgAlaGluLeuSerTyr 172
                                                                                                                       TACGGCGAGTCCCGCCCGGTTGCCGACAACGCCACCGCTGAAGGCCGCGCTATCAACCGT 444
                                                                                                                                            PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                                                                                                                                                    GTTCGTGACGTACTGGTCAACGAGTACGGTGGAAGGTGGTCGCGTGAACGCTGTCGGT
                                                                                                                                                                                        ValArgAsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                                                                                                                ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                                                                                                                                   ThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla 127
                                                                                                                                                                                                                                                            AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                                                                                                {\tt AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis}
                                                                                                                                                                                                                                                                                                                            -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu
                                                                            CGCGTTGAAAGCAGCCAC
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US-09-674-779B-2 (1-172) x AAQ54144 (1-4274)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of plasmid pRW3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid pRW3 contains the whole P.aeruginosa outer membrane protu-
oprF gene with a mutated promoter in pTZ19R. It was isolated for
the creation of OprF epitope insertion vectors which include a
promoter and a DNA sequence encoding at least the amino terminal
portion of a P.aeruginosa OprF. Inserted in the DNA sequence are
one or more unique restriction sites for insertion of one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequences encoding a protein or interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3252 CTGGCCTGGGCGTCGGCTTCAACTTCGGTGGTTCGAAAGCCGCTCCGGCTCCGGAACCGG
                                                                                                                                                                                                                                   78 GluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 IleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys 26
MetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys---Gly
                                                                                                                                                                               AAGGTCAAAGAGAACAGCTACGCTGACATCAAGAACCTGGCTGACTTCATGAAGCAGTAC 3532
                                                                                                                                                                                                                                                                                                    CCGGCTGTCGCCGAAGTCGTACGCGTACAGCTGGACGTGAAGTTCGACTTCGACAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                     ACAAC-GTCGACAAGTGCCCGGATACCCCGGGCCAACGTCACCGTTGACGCCCAACGGCTGC 3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46
                                                                                                                 GlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsn 117
                                                                                                                                                                                                                                                                                                                                                                 ProSerLeu----
                                                                CCGTCCACTTCCACCACCGTTGAAGGTCACACCGACTCCGTCGGCACCGACGCTTACAAC
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                                                                                                                                                                                                                                                                                                                                                                 -----ValTyrPheAspPheAspSerAsp
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                                                                                                                                  Score:
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                                                     US-09-674-779B-2 (1-172) x AAT32599
                                                                                  Query Match:
DB:
                                                                                                                                              Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                        A cDNA sequence (AAT32599) codes for amino acids 190-350 (AAR99625) of the Pseudomonas aeruginosa ATCC 3334 outer membrane protein F (OprF), i.e. the C-terminal region of protein Protein. It was obtd. by PCR amplification of the OprF gene in plasmid pFSauI (see also AAT32592-93). A hybrid gene between glutathione-s-transferase and the OprF sequence was expressed in Escherichia coli. OprF-OprI (AAT32500) and OprI-OprF (AAT32600) hybrid genes were constructed and the encoded proteins (AAR99626-27) were tested for their efficacy as vaccines against P. aeruginosa infection.
                                                                                                        Local Similarity:
                                                                                                                                                                                 Sequence 486 BP; 109 A; 158 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Von
                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 11-12; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broeker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine; fusion protein; OprF; OprI;
antibody; glutathione~S-transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P. aeruginosa OprF C-terminal region cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT32599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT32599
                                                                                                                                                                                                                                                                                                                                                                                                                                             Specht BU;
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                                                                                                                                                                                                                                                                                                                                                                                                       1996-279559/29.
DB; AAR99625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
        32
                                                                                                                                                                                                                                                                                                                                                                proteins for Pseudomonas aeruginosa vaccines nts of outer membrane proteins I and F.
GCTCCGACTCCGACAACGACGGCGTCTGCGACAAC-GTCGACAAGTGCCCGGACACCCCG
                        AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCACCGCTGAAGGCCGCGCTATCAACCGTCGCGTTGAA 3751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAGAAGGTGGTCGCGTGAACGCTGTTGGTTACGGCGAGTCCCGGCCCGGTTGCCGACAAC 3712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domdey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94EP-0120023
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46.15%
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171.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486
                                                     (1-486)
                                                                                                                                                                                 138 G; 81
                                                                            Gaps:
                                                                                                       Mismatches:
                                                                                                                     Conservative:
                                                                                            Indels:
                                                                                                                                 Matches:
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                                                                                                                                                                                 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       В,
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                                                                                                                                                                                                                                                                                                                                                                            contg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δõ
                                   A cDNA sequence (AAT34419) codes for a fusion (AAR99627) between amino acids 21-83 of the outer membrane protein I (oprI) and amino acids 190-350 of outer membrane protein F (oprF) of Pseudomonas aeruginosa ATCC 33354, the 2 moleties being separated by a dipeptide linker. A glutathione-S-transferase fusion with the hybrid gene was expressed in Escherichia coli and Saccharomyces cerevisiae transformants. The
                                                                                                                               Disclosure; Page 15-16; 23pp; English.
                                                                                                                                                       Fusion proteins for Pseudomonas aeruginosa fragments of outer membrane proteins I and
                                                                                                                                                                                                                                          Broeker M, Do
Von Specht BU;
                                                                                                                                                                                                                                                                                                                                     17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P. aeruginosa OprI-OprF hybrid gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                 (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                           16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                               19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                          EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT34419 standard;
                                                                                                                                                                                                  1996-279559/29
DB; AAR99627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValArgAsnTyrLeuLeuGlyLys----GlyIleAsnGlnAlaSerValGluIleIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACGGCGAGTCCCGGCTTGCCGACACGCCACCGCTGAAGGCCGCGCTATCAACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCGACTCCGTCCGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTGGTCGCGTGAACGCTGTCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluThrValLysAlaLeuAlaSerLysLeuProSerLeu--
                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein; OprF; OprI; outer membrane
glutathione-S-transferase; GST; ds.
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                                                                                                                                                                                                                                                     Domdey
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                                                                                                                                                                                                                                                     Η,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
                                                                                                                                                                                                                                                     Hungerer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 BP.
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                                                                                                                                                           vaccines F.
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oprF-oprI fusion oprI-oprF

hybrid protein was significantly less immunogenic than fusion (AAR99626).

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                                                                                                                                                                                                                     DE3718591-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane protein F; OMPF; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane protein F of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN82023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN82023 standard; DNA; 1253
                                                                        03-JUN-1987;
                                                                                                                        03-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
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                         (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                       15-DEC-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGACGTGAAGTTCGACTTCGACAAGTCCAAAGGTCAAAGAGAACAGCTACGCTGACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The protein is isolated from the OMP of P. aeruginosa serotype 6 ATTCC 33354) and purified by HPLC. The amino-terminal and trypsin fragments are sequenced and a series of oligonucleotide probes constructed corresponding to the established sequences. These probes used to screen a gene bank of 15-20 kb fragments of genomic DNA in lambda EMBL 3. One positive clone includes a 15 kb insert conty. the protein gene, which can be isolated as a 2.5 kb PstI fragment. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment cannot be cloned int a high copy no. vector because of the toxicity of the gene prod.., so is subcloned as two fragments with an overlapping region of about 500bp. Ab's are raised by usual immunisation or cell-fusion procedures. The DNA is useful in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domdey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; ; p; German.
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                                                                             1021
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                                                                                                                                                                                                                  ValArgAsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGACGTGAAGTTCGACTTCGACAAGTCCAAGGTCAAAGAGAACAGCTACGCTGACATC
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                                                                             TACGGCGAGTCCCGCCCGGTTGCCGACAACGCCACCGCTGAAGGCCGCGCTATCAACCGT
                                                                                                                          {\tt PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg}
                                                                                                                                                                            GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTGGTCGCGTGAACGCTGTCGGT
                                                                                                                                                                                                                                                                         ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                                                                                                                                                                                                                    ThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla
                                                                                                                                                                                                                                                                                                                                                                    AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                 AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu
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840

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36

127 900

960

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Best Local Similarity:
                                Percent Similarity:
                                                                                                      Alignment Scores:
                                                                                                                                                                                      CC membrane protein, CompA2, from Actinobacillus pleuropneumoniae (APP)
CC strain p2420 (ATCC 98930). The invention relates to the novel APP outer
CC membrane proteins Omp210, OmpA1 and OmpA2 (AAY97996-y97900)
CC and to nucleic acids encoding them (AAA38554-A38589). APP is a Gram
CC negative coccobacillus which is one of the most important swine
CC pneumonic pathogens. 12 different serotypes of APP have been recognised
CC which vary in geographic distribution. Prior art attempts at vaccinating
CC against APP have produced mainly serotype-specific immune responses. In
CC contrast, natural immunity to any one serotype seems to confer
CC significant protection from disease caused by other serotypes, suggesting
CC The novel outer membrane proteins of the invention are present in all 12
CS errotypes, and may provide a target for cross-protective immunity to shared antigens.
CC The novel outer membrane proteins and nucleic acids encoding them can be
CC used as a vaccine against APP in swine. They can also be used as
CX reagents for the diagnosis of APP infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
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                                                                                                                                                Sequence 1319 BP; 428 A; 252 C; 260 G; 379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents DNA encoding a low molecular weight outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 32; Page 49-51; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA encoding them, for use as vaccines against the bacteria in swine - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinobacillus pleuropneumoniae ompA2 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PFIZ ) PFIZER PROD INC
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LM, Suiter BT;
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254..1303
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297..253
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Claim 7; Pages 306-308; 322pp; English
                                                                Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infection
                                                                                                                                                                                                                                                                                                              09-APR-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virulence gene #71
                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                 Lowery DE, Fuller TE,
                                                                                                                                                                                                                                                              (PHAA ) PHARMACIA & UPJOHN INC
                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2000; 2000WO-US09218.
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99US-0153453
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21
                                                                   attenuated vaccine against bacterial infections
                                                                                                                                                                                                                 Kennedy
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                                                                                              stem_loop
                                                                                                                                                                                                                                                                                                                Fimbrin protein; vaccine; otitis media;
                                                                                                                                                                                                                                                                                                                                                             Non-typable
                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-1995
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                           WO9426304-A
                                                                                                                                                                                                                                                                   Haemophilus
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                                                                                                                                                                                                                                                                   influenza strain 1128.
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typable clinical isolates of Haemophilus influenzae share common
epitopes. Thus frimbrin isolated from non-typable Haemophilus
influenzae 1128 Strain is a particularly suitable immunogen to
protect against the different non-typable HJ. influenzae that cause
otitis media. Fimbrin protein is produced by culturing a transformed
microbial host, pref. E.coli, Sporodoptera frugiperda or a mucosal
pathogen. Fimbrin protein (FP) produced by this process is claimed.
The FP protein migrates in polyacrylamide genes to a posn. equiv. to
a mol. wt. of 25.5 kD or 37.5 kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 ProAsnAlaProThrGlyTyr-----
                                                                                                                                                                                                                                                                                                                                 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg
  CGTAAAGCACTTATCGCTTGTCTTGCTCCAGACCGTCGTGTAGAAATCGCA 1467
                                                                                                                                                                                                                                        ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu
                                                                                                                                                                                                                                                                                                                                                                                      CAAGCTACATTAGACAGCGTCTATGGCGAAATTTCACAAGTTAAAAGTCGAAAAGTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGC --- TTAAATTCTGATGTAACTTTCGCATTTGGTAAAGCAAACTTAAAACCTCAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAla
                                                                                                                                              IleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu-----
                                                                                                                                                                                                CGTGCAGATTCAGTAGCTAACTACTTTGTTGCTAAAGGTGTTGCAGCAGACGCAATCTCA 1356
                                                                                                                                                                                                                                                                                         GTTGCTGGTTACACTAACCGTATTGGTTCTGACGCGTTCAACGTAAAACTTTCTCAAGAA 1296
                                                                                              GCAACTGGTTACGGTGAAGCAAACCCAGTAACTGGCGCAACTTGTGACCAAGTTAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 5; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 571 A;
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165.50
46.50%
29.94%
19.22%
                                            ----AlaTrpSerGlnAsnArgArgAlaGluLeuSer 171
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Matches:
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Indels:
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Pred.
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AAL46503
               Alignment Scores:
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05-SEP-2000;
05-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
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29-AUG-2000;
29-AUG-2000;
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28-AUG-2000;
28-AUG-2000;
                                               The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a coding sequence of the invention.
      No.:
                                  Sequence 898
                                                                                                                Claim
                                                                                                                               Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria
                                                                                                                                                                                                                        (AVET
                                                                                                                                                                                                                                                              05-SEP-2000;
06-SEP-2000;
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01-SEP-2000;
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29-AUG-2000;
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29-AUG-2000;
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29-AUG-2000;
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                                                                                                                                                                                                     Loosmore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL46503
                                                                                                                                                                                 2002-401721/43.
                                                                                                             2; Fig 21; 277pp; English.
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2000US-228295P

2000US-228439P

2000US-228441P

2000US-228442P

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2000US-228442P

2000US-228472P

2000US-228511P

2000US-228772P

2000US-228773P

2000US-228774P

2000US-229474P

2000US-229478P

2000US-229803P

2000US-229803P

2000US-229803P

2000US-239803P

2000US-239803P
                                  BP;
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                                 290 A; 171 C;
      1.75e-10
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Best Local Similarity:
The present invention relates to a Moraxella catarrhalis genomic library
                                                                                                                                                                                                                                                                                                                  AAF28548;
                                         acids
                                                                                                                                                 18-JUN-1999;
                                                                                                                                                                                       28-DEC-2000.
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US-09-674-779B-2 (1-172) x AAL46503 (1-898)
                                                                                                                                                    Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucle
Claim 1; Page 345-368; 545pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic library; bacteria; human upper airway; otitis media; bronchopulmonary; endocarditis; meningitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 96109 BP; 28783 A; 18910 C;
                   mat_peptide
                                                     sig_peptide
                                                                                                                                                                                            Haemagglutinin; antigen; vaccine;
hagA; gene; ds.
                                                                                                                                                                                                                                              Haemophilus
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                                                                                                                                                                                                                                                                                                                   ABA91419
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                                                                                                                                                          Haemophilus paragallinarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGCATGAGTATAATCAAGATTTATCAGAATCTCGTGCTGCTGCTGTTAAAGAGTATTTG
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                                                                                                                                                                                                                                             paragallinarum strain 2403 haemagglutinin hagA gene
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                                                                       "haemagglutinin"
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                                                                                                                                                                                                            coryza; chicken;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 other;
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Query Match:
                                 Percent Similarity:
Best Local Similarity:
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                                                                                                     Alignment Scores:
                                                                                                                                                                                     The present sequence is that of the coding region of the hagA gene CC of Haemophilus paragallinarum strain 2403 (serovar A). The gene CC was isolated from chromosomal DNA by PCR amplification. It encodes haemagglutinin (see AAM50718). The invention provides cencodes haemagglutinin (see AAM50718). The invention provides cencoding nucleic acids (see AAM501417-27) from 11 strains (serovars A, B and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for coryza of chickens. The polypeptides are useful in vaccines for mmunisation against infectious coryza, as are the nucleic acids when expressed in attenuated bacteria, especially Salmonella or CC wropalsama (claimed). The recombinant polypeptide is preferably the mature protein, or a biologically active fragment, variant or CC derivative, that is capable of eliciting an immune response, providing protection against one or more strains of H. CC paragallinarum in chickens. Also claimed are methods of using the haemagglutinin polypeptides and nucleic acids for detection and
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No.:
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                                                                                                                                        Sequence 1035 BP; 319 A; 186 C;
                                                                                                                                                                          diagnosis of infectious coryza in chickens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 5; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAM50718.
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                                   Mismatches:
Gaps:
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US-09-674-779B-2 (1-172) x ABA91419 (1-1035)

ΟУ 116 Тγ	Db 769	Qy 96 Th	Db 715 Cc	Оу 80 Гу	Db 661 AP	Qy 60 Ly	Db 601 GC	Qy 42 Th	Db 541 GG	_
116 TyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys 135	769AAATCAGTACAAGTAGATGTTGCTGGTTATACTGACCGTATTGGTAGCGAAGCA 822	96 ThrasnGlnThralaArgValLeuValAlaGlyHisThraspGluArgGlySerArgGlu 115	GTATTTATGGT	80 LysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThr 95	661 AAAACATTTGCATTAAATTCAGATGTTACTTTCGCATTTGGTAAAGCAAATTTA 714	60 LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle 79	601 GCTGGTTTATCTTACCGTTTTGGTCAAAGTGCACCAGTTGTTGAACCTAAGGTTGTTGCA 660	42 ThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrVal 59	541 GGACGTGTGGAAAAAGATGGTAGCCGTGTAGATTATACACCAAGCATCGGTTCTGTAACT 808	TO THE CONTRACT OF THE PROPERTY OF THE PROPERT
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    The present sequence is that of the coding region of the hagA gene of Haemophilus paragallinarum strain 0222 (serovar B). The gene was isolated from chromosomal DNA by PCR amplification. It encodes haemagglutinin (see AAM50721). The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-27) from 11 strains (serovars A, B and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for when expressed in attenuated bacteria, especially Salmonella or Mycoplasma (claimed). The recombinant polypeptide is preferably the mature protein, or a biologically active fragment, variant or derivative, that is capable of eliciting an immune response,
                                                                                                                                                                                                                      Claim 11; Fig 5; 67pp; English.
                                                                                                                                                                                                                                                            New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                                                                                                                                                P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                         Tseng H,
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   eliciting an immune response,
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   sig_peptide
                                                                                                                                Haemagglutinin; antigen; vaccine; immunisation; coryza; chicken;
                                                                                                                                                           Haemophilus paragallinarum strain 2671 haemagglutinin hagA gene
                                                                                                                                                                                                                             ABA91423;
                                                                                                                                                                                                                                                       ABA91423 standard; DNA; 1035
                                                                                          Haemophilus
                                                                                                                        hagA; gene;
                                                                                                                                                                                                 18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                providing protection against one or more strains of H. paragallinarum in chickens. Also claimed are methods of using haemaggluthin polypeptides and nucleic acids for detection and diagnosis of infectious coryza in chickens.
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                                                                                          paragallinarum
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/product= "haemagglutinin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of the coding region of the hagA gene of Haemophilus paragallinarum strain 2671 (serovar B). The gene was isolated from chromosomal DNA by PCR amplification. It encodes haemagglutinin (see AAM50722). The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-27) from 11 strains (serovars encoding nucleic acids (see ABA91417-27) from 11 strains (serovars and C) of H. paragallinarum, the causative agent of infectious A, B and C) of H. paragallinarum, the causative agent of infectious A.
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                                                                                                                                                 LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle 79
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                                                                                                                                                                                                                                                             GGACGTGTGGAAAAAGATGGTAGCCGTGTAGATTATACACCAAGCATCGGTTCTGTAACT 600
ThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGlu 115
                                                CGTCCAGAAGCACAAAATGTATTAGACGGTATTTATGGTGAAATCGCACAGTTA-----
                                                                                 LysProGlnAlaAlaAlaIleLeuAsp-----
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64..1032
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ID ABA91
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   The present sequence is that of the coding region of the hagA gene of Haemophilus paragallinarum strain H-18 (serovar C). The gene was isolated from chromosomal DNA by PCR amplification. It encodes haemagglutinin (see AAM50724). The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-27) from 11 strains (serovars A, B and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for immunisation against infectious coryza, as are the nucleic acids when expressed in attenuated bacteria, especially Salmonella or
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hagA; gene; ds.
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                                                                                                                                                                    Claim 11; Fig 5; 67pp; English.
                                                                                                                                                                                                                New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
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Command line parameters:

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-Q-/cgn2_1/USPTO_spool/US09674779/runat_06072003_121614_9813/app_query.fasta_1.327
-DB=EST -OFMT-fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALION=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
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-USER=US09674779_eCGN_1_1_1525_eTunat_06072003_121614_9813 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6
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SUMMARIES

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                                                                                                                                          White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                       BE530264 247 bp mRNA linear EST 19-MAR-. M77K09STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone 600039738R1 5', mRNA sequence.
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;;;;,
Clones were originally prepared at Michigan State University. Arabidopsis Biological Resource Center, The Ohio State University, 309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
                                                              Tel: 517 355 1609
Fax: 517 353 9334
                                                                                                                          Contact:
                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Enassicaceae; Arabidopsis.
                                                                                                                                                                                                                                         Arabidopsis thaliana
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                                                                                                       Michigan State University
                                                                                                                                     20567808
                                                   Email: benning@msu.edu
                                                                                            224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                   USA
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                                                                                                                ct: Benning, C
  of Biochemistry & Molecular Biology
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BI118605 602912021
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RESULT 2
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                                                                                                                                                                                                                                                                                          Unpublished (2001)
Other_GSSs: AG-ND-131G1.TF
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 779)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J. Direct Submission of BAC-end sequences from Anopheles gambiae
to minimize the inclusion of DNA from microorganisms that inhab the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a Hind.
                                                                               This clone is from an A gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TICR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae
                                                                                                                                                                                  9712 Medical Center Dr., Rockville, Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG-ND-131G1.TR ND-TAM Anopheles DNA sequence.
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                                                                                                                                                                   bjloftus@tigr.org
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/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
site_1: EcoRI; Site_2: 64 t
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="600039738A1"
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Seq primer: M13
Class: BAC ends.
                                                       Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                       NF106A12DT1F1087 Drought Medicago truncatula cDNA clone 5', mRNA sequence.
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Flores, H.R., Inman, J.T., Weller, J.W. and
                                                                                                                                                      EST
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                                                                                                                                     barrel medic.
                                                                                                                                                                  BF635668.1 GI:11899826
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                                (bases 1 to 236)
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ss: BAC ends.
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/note="Vector: pECBAC1;
115 c 163 g 19
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/clone="AG-ND-131G1"
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/strain="PEST"
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                 Bell, C.J.,
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Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
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                                                                                                                               Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
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Tel: 580 221 7391
Fax: 580 221 7380
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The Samuel Roberts Noble Foundation
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Insert Length: 236 Std Error: 0.0
Plate: 106 row: A column: 12
Seq primer: TCACACAGGAAACAGCTATGAC
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/db_xref="taxon:3880"
/clone="NF106A12DT"
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/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
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                 Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 099 row: G column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                          Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                         Medicago truncatula drought library Unpublished (2000)
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5', mRNA sequence.
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Insert Length: 246 Std Error: 0.0
Plate: 092 row: B column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
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/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
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                                                                                                                                                                                                                                                                                                                 Fax: (44) 122 721 Particular Fax: (44) 127 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ990953 14-AUG Rfc01801 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01801, DNA sequence.
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone_lib="Drought"
/tissue_type="Plantlets"
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/note="Vector: Lambda Zap; Contains a mixture of entire
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
On Jul 13, 2000 th
                                                                                                                                                 Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzal Flores,H.R., Inman,J.T., Weller,J.W. and May,G.Expressed Sequence Tags from the Samuel Roberts
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                                                Plant Biology Division
The Samuel Roberts Noble Foundation
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118 c 137 g 145 t 3 others
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Shetty,J., Malek,J., Koo,H.,
Direct Submission of BAC-end
Unpublished (2001)
Other_GSSs: AG-ND-126C17.TF
                This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC
                                                                                                                                                        9712 Medical Center Dr., Rockville, Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                       Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: gdmay@noble.org
library was constructed at Texas A&M Universty BAC Center
                                                                                                                                    Email: bjloftus@tigr.org
                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH404849.1 GI:17351065
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                                                                                                                                                                                                                    Institute for Genomic Research
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/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture
plantlets harvested in a series of days-post-w
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Seq primer: M13
Class: BAC ends
                       The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA 19712 Medical Center Dr
                                                                                                                                                                                                                               Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                             Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                           Other_GSSs: AG-ND-160F6.TF
                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 603)
Shetty, J., Malek, J., Koo, H.,
Direct Submission of BAC-end
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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(TIGR). The BAC library was generated from A. gambiae PEST strain
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/clone="AG-ND-126C17"
/clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: pECBAC1; Site_1: HindIII"
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/strain="PEST"
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US-09-674-779B-2 (1-172) x BH403497 (1-603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 PheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPhe 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAsp 73
                                                                       The
                                                                                                                                                           1 (bases 1 to 814)
Shetty, J., Malek, J., Koo, H.,
Direct Submission of BAC-end
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH386478 814 bp
AG-ND-170A18.TF ND-TAM Anopheles
                                                                                                                                                                                                                                                                                                   Anopheles gambiae
Eukaryota; Metazoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BNC library was constructed at Texas A&M Universty BAC Center
                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                Contact: Brendan J Loftus
                                                                                                                                   Other_GSSs: AG-ND-170A18.TR
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                                                                                                                                                                                                                                                                           Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                 African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySer 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTAATAAAGCAACAATAACAAATGAGTCAGGTGCAAAGCTAGATGTAGCTGCCAACATT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGCATACAACCTTAAGCTTTCCAGAGAAAGAGCGGCTGCTGTTGTTGGAGCTCTGGAA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeu 133
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Medical Center Dr., Rockville, 301 838 0208 301 838 3543
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1;
a 81 c 151 g 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .603
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                                                                                                                                                                                                                                                                              Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
Indopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126.00
55.56%
32.22%
14.63%
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                                                                                                                                                                  Collins,F., Garumer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gambiae genomic clone AG-ND-170A18
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                                               20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                     gambiae
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BASE COUNT
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                                                     REFERENCE
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       AUTHORS
TITLE
                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 GluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 GluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590 AAAGCTCTTGAAGCTAGAGGTGTAAACGGTGCTCAATTGAAATCTGTAAGTGTAGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                      710 GAAGTG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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  Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
                                                                                                                                          Anopheles gambiae
                                                                                                                                                                                                                BH374389.1 GI:17320531
                                                                                                                                                                                                                                      вн374389
                                                                                                                                                                                                                                                                                  BH374389 512 bp
AG-ND-177A3.TF ND-TAM Anopheles
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                                                                                                                                                                African malaria mosquito
                                                                                                                                                                                                                                                         DNA sequence.
                                                                                            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                      Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGAAGCTACTGTACCAGCTACTGCTTCTTACGAGGCTAGACAAGTAGACAGAAAAGTT 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTAAAGGTAATCCTAACTACAACTTGAAATTATCAAGAGAAAGAGCTTCTTCTGTAGTT 589
                                              (bases 1 to 512)
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: PECBAC1; 214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Anopheles gambiae"
/strain="PEST"
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                                                                                                               Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Collins, F., Gardner, M. and Loftu sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                  gambiae genomic
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                          Gardner, M. and Loftus, B.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 TTTAATAAAGCAACAATAACAAATGAGTCAGGTGCAAAGCTAGATGTAGCTGCCAACATT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 GACAATAACCAGGTTGCAACTGAAGTAGAAACAGAATTAAAAAAT---GTGTATTTCCAT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468 GCTAGAGGAGTTTCTTCCCAGACTCTTAAA 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74\ Phe Asp Ser Asp Glu Il e Lys Pro Gln Ala Ala Il e Leu Asp Glu Gln Ala Gln Phe Asp Ser Asp Glu Il e Lys Pro Gln Ala Ala Il e Leu Asp Glu Gln Ala Gln Phe Asp Ser Asp Glu Il e Lys Pro Gln Ala Ala Il e Leu Asp Glu Gln Ala Gln Phe Asp Ser Asp Glu Il e Lys Pro Gln Ala Ala Ala Il e Leu Asp Glu Gln Ala Gln Phe Asp Ser Asp Glu Gln Ala Gln Phe Asp Glu Gln Phe Asp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAsp
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                                         Anopheles gambiae
Eukaryota; Metazo
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Fax: 301 838 3543
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Department of Eukaryotic Genomics
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Other_GSSs: AG-ND-177A3.TR
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                              African malaria mosquito.
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                                                                                                                                                                                                                                                                          DNA sequence.
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/note="Vector: pECBAC1;
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/strain="PEST"
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                                                                                                                                                                                                                                                                                                                                          43 GlyVal---IleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAla
                                                                                                                                                                                                                                                                                 62 LeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 838 0208
Fax: 301 838 3543
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Department of Eukaryotic Genomics
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ACTACAAACAAAAGGTTTTGGACAGGATAATCCTTTGGCT
                                                            ATTGGACAGAGCTACAACAATATACTTATTTAACAGATAAAGGGATTAAATCTGATAG
                                                                                        yGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSe
                                                                                                                         CTTTCTATAGAAGGGCATACTGACAACAATGGTACAAAAGAACACAATTAGGAAATTATC
                                                                                                                                                      ValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsn-MetSerLeuGl
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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/strain="PEST"
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US-09-674-779B-2 (1-172) x BH393516 (1-822)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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The Institute for Genomic Research
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Other_GSSs: AG-ND-160N3.TF
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Class: BAC ends.
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Fax: 301 838 3543
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                                 ArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeu 133
                                                                                                                                                                                                                                                                                                                                                    GluThrValLysAlaLeuAlaSerLysLeuProSer------LeuValTyrPheAsp 73
GCAGCATACAACCTTAAGCTTTCCAGAGAAAGAGCGGCTGCTGTTGTTGGAGCTCTGGAA 463
                                                                                                                                                                                                                                                             PheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPhe 93
                                                                                                                                                         LeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySer 113
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1;
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                                110 GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                                                               275 GTGTATTTCCATTTTAATAAAGCAACAATAACAAATGAGTCAGGTGCAAAAGCTAGATGTA 334
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                                                                                                                                 90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                      70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
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Other_GSSs: AG-ND-132E3.TF
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan J Loftus
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AG-ND-132E3.TR ND-TAM Anopheles
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GCTAAAGGTAGTGCAGCATACAACCTTAAGCTTTCCAGAGAAAGAGCGGCTGCTGTTGTT 451
                                                                                         GCTGCCAACATTATTAAGAGCAAT----GGTGGAAATTATCTATTAACCGGACATACAGAT
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/note="Vector: pECBAC1; Site_1: HindIII"
100 c 169 g 205 t
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                                                                                                                                                                               39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
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Fax: 301 838 3543
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other_GSSs: AG-ND-155H3.TR
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GCGGTTAACCGATATCTACAGTCAAAAATTGGAAACAATATCAAACTGGAAAGTGTAGTA
                                                                                                                              HisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal 126
                                                                                                                                                                          CTCGACAGTTTGGCGCAA----CTTAGATATAATCTGAAATTCAGAATTTTT------GGA
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                                       AlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu---IleIle 145
                                                                                     AATTGCGATATTTCCGGAACTTTGGAATACAATAAAAAGCTGTCTGAAAATCGCGCAAAT 149
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/clone="AG-ND-155H3"
/clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
a 71 c 96 g 114 t
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                                                           90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microGraanisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University, College Station, Texas 77843-2123, USA using a HindIII
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH376004.1 GI:17322146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG-ND-135A18.TR ND-TAM Anopheles gambiae genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  partial digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                        GCTGCTGAGATTATCAAAGGAGCTAAAGCTGAAAACTTCTTAGTAACTGGTTACACAGAT
                                                                                                                                      ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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/note="Vector: pECB!
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/db_xref="taxon:7165"
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                         Similarity:
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                                                                                                                                                                                                                                    70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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327H1B83102397 Cosmid library of chromosome II Rhodobacter
sphaeroides genomic clone 8327H1B83102397, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6431 fannin Street, Houston,
Tel: 713 500 5437
Fax: 713 500 5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RsGDB, the Rhodobacter sphaeroides Genome Database Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choudhary, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Microbiology and Molecular Genetics
University of Texas Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: madhu@utmmg.med.uth.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Choudhary, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter.
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AsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSerPheGly
                                                                             GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                                           GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
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                                          GCGGCGGGCAGCCAACCAACCAGCAGCTCTCGCTCCTGCGGGCCGAGGAGGTGCGC
                                                                                                                      CTCTGCACGGTGATGAAGGCGAGCGACATCCGCCTGTTTCAGATCGTGGGCCACACCGAT
                                                                                                                                                                                                  ATCCATTTCGCCTTCGACTCGGCGGTGCTGGCCGCGGATCAGACGCCGCTTCTCGCGCAG 148
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/clone="8327H1B83102397"
/clone_lib="Cosmid library o
/lab_host="F. coli $17-1"
/note="Vector: pLA2917"
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/strain="2.4.1T"
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RESULT 18
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                                                                 234 GACAATAACCAGGTTGCAACTGAAGTAGAAACAGAATTAAAAAAAT---GTGTATTTCCAT 290
74 PheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPhe 93
                                                                                                                   54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAsp 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University. College Station, Texas 77843-2123, USA using a HindIII partial digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftu: Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2011)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence.
BH393822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            African malaria mosquito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-169D8"
/clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Yector: pECBAC1; Site_1: HindIII"
89 c 151 g 184 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=ILst2=IL-BT042-008.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                         716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. **

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; SmaI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 379
High quality sequence stop: 585.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM12285 row
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                                                                                                                                                                                                                                                             344
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                                                                                                                                                                                                                                                             മ
                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pcMV-SPORT6;
Site_1: Not1; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones donstructed by Life
Technologies. Note: this is a NIH_MGC Library."
a 277 c 241 g 273 t 17 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:5560157"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                  3.75
86.50
48.33%
25.00%
10.05%
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AUTHORS
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      626 CCAAGCAATGAATTCCTTGGCAGCTTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 ArgProIleAlaPheGlyThrAsnGlu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 GlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                785 TTGGTCTGAATCAACCAGTTTATAAAGTCCCTGGCGGCAAGATTATCAAGAATGGTGTTC
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
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Contact: Tadasu Shin-i
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Ogihara, Y. and Murai, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed genes in Triticum aestivum
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                       138
                     Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)." a 233 c 181 g 132 t 2 others
                                                                                      library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chir Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
                                                                                                                                                                                                                                                   /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: ECORI; Site_2: XhOI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov
                                                                                                                                                                                samples, polyA was purified from the pooled RNA, a cDNA
                                                                                                                                                                                                      in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two
                                                                                                                                                                                                                                                                                                                                              /clone_lib="Y. Ogihara unpublished cDNA library, Wh_SL"
/tissue_type="seed DPA30"
/dev_stage="Feekes' scale 11.3"
                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whs120n03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
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...
                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 GATGAGTTGGCCGTTGAGGGAAAGGGCCTTGGACGCGGCATCAGGGCTCGCGAAGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
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Shetty,J., Malek,J., Koo,H.,
Direct Submission of BAC-end
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          partial digest.
                                                                                                                                                                                                                                                                                              Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Other_GSSs: AG-ND-126A8.TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AGCAAGACCACCACCAGGGCCCAGTTCAGCTTGAAAGGGCGGTTGGAGTTGGG 134
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Unpublished
                    University
                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                    Maize ESTs from various cDNA libraries sequenced at Stanford
                                                        Walbot, V.
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/clone="AG-ND-126A8"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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plate: 952035 row: D column:
Location/Qualifiers
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                                                                                                                                                                                                     MetSerLeuGlyGluArgArgAlaVal-AlaValArgAsnTyrLeuLeuGlyLysGlyIl 137
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                                                                                                                                                                                                                                                                                                                                      TTGCTGGATGAACAATTTGATTTGCTTGCTTTGGAGGAA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligo(dT) primers in separate reactions and equipped with
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/db_xref="taxon:4577"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu 66
                                                     96 ThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCOURT_8192156 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6260167 5', mRNA sequence.
BQ678932
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLCM2418 row: n column: 08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
ACTAGTGCAACCAGTAAGTTGATC-----CATCCAGATGAG---
                                                                                                                AGTACTGCAGCTAAACCA----GCGGCTTCAATAACAAGTAAGCCTGCTACACTTACAACA 676
                                                                                                                                                                  SerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThr 95
                                                                                                                                                                                                                                       CCAAAGCCTACATTCCCTGCTTATACACAGTCTACAGCTTCAACAACTAGTACAACAAAT 619
                                                                                                                                                                                                                                                                                                   ProSerLeuValTyrPheAspPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

283 c 186 g 193 t 2 others
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/lab_host="PHIOB (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5; adaptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:6260167"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_112"
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Qy	Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match: DB: US-09-674-779B-2 Qy 9 Al	BASE COUNT	FEATURES Source		AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 25 BM448527 LOCUS DEFINITION	Qy	Qy Db
	: 5.86 Length: 565 ty: 41.33% Conservative: 26 arity: 24.00% Mismatches: 54 9.41% Indels: 34 13 Gaps: 5 (1-172) x BM448527 (1-565) aalaalaalaalaalaeuServalLeuThrPheMetThrGlyCysAlaAsnLysSerThr[]	/CLONE="USAUZ2BU3" /CLONE="USAUZ2BU3" /CLONE="Lib="Nn expressed sequence tag database for the halotolerant green alga, Dunaliella salina" /tissue_type="Cells, which was adapted in 2.5M NaCI via a incremental series from 1.7 to 2.0 to 2.25 to 2.5 M NaCI, were exposed to 3.4 M NaCl for 5 hours" /cell_type="Green" /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: ECORI; Site_1: XhOI: Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."  131 a 163 c 179 g 92 t	High quali	Department of Biochemistry University of Nevada MS200, Reno, NV 89557-0014, USA Tel: 775-784-1918 Fax: 775-784-1650 Email: jcushman@unr.edu PCR PRimers FORWARD: T3 20mer BACKWARD: T7 21mer Plate: 025 row: B column: 03	Cushman, J.C. An expressed sequence tag database for the halotolerant green alga, Dunaliella salina Unpublished (2002) Contact: Cushman JC	BM448527 BM448527.1 GI:19854099 EST. Dunaliella salina. Dunaliella salina Eukaryota; Viridiplantae Dunaliellaceae; Dunaliel		135 sGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro 152 750AGTATCAACGTAATCTTCCTCGGCCAGGACAGGCCC 785	116 TyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn-TyrLeuLeuGlyLy 135 ::::::
Alignment: Pred. No.: Score:	BASE COUNT	FEATURES SOUTCE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	BE372739 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM		0 0 0 0 V	рь Оу	Db Qy	Ωb .
Scores: 6.84 Length: 620 81.00 Matches: 41	/strain="FVB/N" /db_xref="taxon:10090" /dlone=Tib="MAGE:382660" /clone=Tib="NCI_CGAP_Mam1" /tissue_type="tumor, biopsy sample" /tissue_type="tumor, biopsy sample" /dev_stage="10 months, virgin" /lab_host="DH10B" /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Oligo dT. site_2: Not; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator .providing samples: Gilbert Smith, NIH"  137 a 179 c 175 g 129 t	Email: cgabbs-r Tissue Procurem CDNA Library P CDNA Library A DNA Sequencing Clone distribu found through t http://image.ll Plate: LIAM8738 High quality se Locati 162	ROGENTIA; nci.nih.gov of Health ausberg, Pl	BE372739  620 bp mRNA linear EST 21-JUL-2000 601224250F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3582660 5', mRNA sequence.  BE372739  BE372739.1 GI:9318102  EST. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	141 SerValGluIleIleSerPheGlyGluGlu 150 ::::::         :::	101 ArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeu 120	119 GCAGAGGTGGAGGGCGAGGCCCTTGGCCAGGAGTTCAAGGGATACATTTTCAAGATCATG 178  88AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAla 100	71ATCGATGATGACGCCAAGCTGCTGCGCCTTCTACGACAAGCGCCTGTCC 118 68 SerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaAlaLleLeu 87	70 70 49 ValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuPro 67

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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSerGlnValMetVal
                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1591)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                              Plate: LLCM753 row: a column:
                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                 High quality sequence stop: 60.
                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory
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/tissue_type="melanotic melanoma"
   /lab_host="DH10B (phage-resistant)"
                                                                 /db_xref="taxon:9606"
                                                                                  /organism="Homo sapiens"
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                                                  AUTHORS
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l (bases 1 to 458)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
                                                                                                                                                                             BF758001 458 bp mR1
QV3-CT0555-101100-369-e01 CT0555 Homo
BF758001
                                                                                                                                              BF758001.1
EST.
                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                              Homo sapiens
                                                                                                                                 human.
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GI:12105901

mRNA

sapiens

cDNA,

mRNA sequence.

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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US-09-674-779B-2 (1-172) x BE729857 (1-1591)
                                                                                                                                                                                                                                                          544 CAGTGCGCCTTTTCTGAGAGAGTGTCACTAACACCCTTGGCTCTCACCACGGCCGCAGAG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                110 luArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal------
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424 ACACACAC-----AGCTGGGGTGTCTCCCGCGGAGAGGAGTCTTCC
                                                      156 lyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               826 GGGGATAAAATTTGCTCCTCGCCGCCCCAACTATACTGCGGCGGTTGTTCCTCTTCGCGA 767
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                                                                                                                         TGATACACCCTCTCGGCCACGCGTGTCTCTTTGGGTTGAGAACGCCCCACTTCACTTC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGTGAGAATTGCATCACGCGCGCTCCCCGCGAGACTCACACGCTTGGGGGCACAGA---G
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    ACCESSION
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-CT0555-
101100-369-e01&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
908 bp mRNA linear E AGENCOURT_7575827 NIH_MGC_72 Homo sapiens CDNA clone 5', mRNA sequence.
BQ218323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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                                                                                                                                              AGG 127
                                                                                                                                                                                  Lys 135
                                                                                                                                                                                                                             GCAAAACAGAGTCGGAGTGAAAAGAAGGCACGGAAGGCTATGTCCAACTGGGTCTTCGGC 130
                                                                                                                                                                                                                                                                 TyrAsnMetSerLeuGlyGluArgArgAla---ValAlaValArgAsnTyrLeuLeuGly 134
                                                                                                                                                                                                                                                                                                                                                  ThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGlu 115
                                                                                                                                                                                                                                                                                                                                                                                             AGTGATGAATCAGTACCAGAG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Adult"
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    325 AGAGCGAGAGATCAAAGAAAGAATAGAACGAGTTAAGAAGGCCTCGAGAAGAGCATGAGAG
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                                                                                     265 AGTTCAACCTAGGGCACAGAAAATTGCAGAACATCGGAGAAAGTATGAGCGAAAACGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                  43 AAGGAAGATGGCGGATCTGGAGGAGCAGTTGTCTGATGAAGAGAAGGTGCGTATAGCAGC 102
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EST.
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Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                         uIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGl 98
                                                                                                                                                                      TAAATTG------GATTATGATGAAGATGCTAGTGCAATGCTGAAAGA 264
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo c
Sverage insert size 2 kb. Library constructed by Life
Technologies."
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/clone="IMAGE:6047154"
/clone_lib="NIH_MGC_72"
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497 GGCGACCTCTTCTGGGAAATCTCGCCTTCCTCG-
                                                                                                                                                                                                                                                 671 CAGGTGATGTTGTGAAGAGGATCTTGAATAGGTGATATAGTTATTTTCCTGTCAGGGATT
                                     90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                       50 AlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu 69
                                                                                                                      70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BM475133
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/lab_host="DB10B (phage_resistant)"
/note="organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), for the continuous constitution of the constitutio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1794 row: c column: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

277 c 359 g 253 t
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/lab_host="DH10B"
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29 SerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGly 48

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AQ847628.1
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ847628 385 bp DNA linear GSS 25-MAY-2 LMAJFV1_lm35c11.yl Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm35c11 5', DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashIngton University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                       N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing, and the Washington University Genome Sequencing Center For information on obtaining clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim wustl.edu) and/or Stephen M. Beverley Ph.D.
                                                                                                                                                                                                                                                                                                                                                Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21192569
Contact: Akopyants, NS / Beverley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOL
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Akopyants,N.S., Clifton,S.W., Martin,J., Pape,D., Wylie,T.,
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                                                                                                                                                                                                       Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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                                                                                                                                                                                                                           (beverley@borcim.wustl.edu)
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                                                                                /organism="Leishmania major"
/strain="Friedlin strain Vl"
                                                                                                                                          ity sequence stop: 
Location/Qualifiers
/clone_lib="Leishmania major FV1
/lab_host="TOP10 (Invitrogen)"
                                      /clone="LMAJFV1_lm35c11"
                                                           /db_xref="taxon:5664"
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Euglenozoa; Kinetoplastida; Trypanosomatidae;
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US-09-674-779B-2 (1-172) x AQ847628 (1-385)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 ArgGluTyr---AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE13571 480 bp mRNA linear EST 21-JUN-200 ug53a03.yl Barstead bowel MPLRB9 Mus musculus cDNA clone IMAGE:1546060 5' similar to TR:060817 NG0817 NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE;, mRNA sequence.
                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine
                                                                                                                                                                   1 (bases 1 to 480)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, B. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
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Forest Park Parkway, Box 8501, St. 314 286 1800 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                          ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                     ----GlnAlaSerValGluIleIleSerPheGlyGluGluArg 151
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRÂNCE. (E-mail:
3 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and varrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                     250 ACATTTAGCGGTTGGGCTAGTAACACTACGTCTGAT-----GTAACATCAACAGAG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 487 (1), 66-70 (2000)
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/strain="CLIB 210"
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/clone="BA0AB036F06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 460)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W20805 460 bp mRNA linear EST 10-SEP-19 mb91006:r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:336778 5' similar to PIR:S4926 S49326 Nascent polypeptide associated complex alpha chain - human ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAACCTTCTCATTGACTACTGTCACTACAACAAGTAATGGCATGACC---ACTATTTAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAAGTTCTAGTGTTGAAGTAACAACCGCTTCTCAAAATGCTGAAGTCTCATCAGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrGlyValAlaProLeu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSer 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AlaSerValGluIleIleSerPheGlyGlu-------GluArgPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTTGTCCTATCGATACCACTACCACTGAAAGTGCATCTAATGAGTATCACACTTCAAAG
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                                                                                                                                                                          primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                314 286 1800
314 286 1810
                                                                                                                                                          quality sequence stop: 454
/clone_lib="Soares mouse p3NWF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:1297704
                                                                      /clone="IMAGE:336778"
                                                                                         /db_xref="taxon:10090"
                                                                                                       /organism="Mus musculus"
                                                                                                                                           Location/Qualifiers

    ValAspAsnAspGluThrValLys 60

                                                                                                                                                                                                                                                                                                  Louis,
                                                                                                                                                                                                                                                                                                  MO
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BG261745
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                       COMMENT
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                                                                      AUTHORS
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No.
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 Email: cgapbs-r@mail.nih.gov
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US-09-674-779B-2 (1-172) x W20805 (1-460)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                  402 TACAAGAGCCCAGCTTCAGACACCTACATAGTGTTTGGGGAACCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 CGTTCTCTTCTGCCGCCATCTTGGTTCCGTGATCTCCGCACAAAATGCCCGGT-----
                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
                                                                                                                                                                                                         mRNA sequence.
BG261745
BG261745.1 GI:12771561
                                                                                                                                                                                                                                                                     BG261745 LUBS bp r
602373532F1 NIH_MGC_94 Mus musculus
Contact: Robert Strausberg, Ph.D
                   Unpublished (1999)
                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                             Mus musculus
                                                                                                                                                                      house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgValLeuValAlaGlyHisThrAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgAsnTyrLeuLeuGlyLysGlyIleAsn-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGAGAGTCACTATCCGAAAATCTAAAAATATCCTCTTTGTCATCACAAAACCCGATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                          -----GlnAlaSerValGluIleIleSerPheGlyGluGluArg
                                                                                  (bases 1 to 1083)
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119 c 122 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           normalization to a Cot = 5. Library constructed by Bento
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25.00%
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                                                                                                      Craniata; Veri
Sciurognathi;
                                          Mammalian
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                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                            cDNA clone
                                                                                                      Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                          Gene
                                                                                                                                                                                                                                                                            IMAGE:4481142
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RESULT 37
BE261626
                                REFERENCE
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    AUTHORS
                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 CAAGGGGTAAGAGAAACCCTGGAGAACCTTGGACTTGTCTGGCCACCGGGATTCCAAGGGT
                                                                                                                                                                                                                                                                                                                                                                781 GTTGGTGGCGGGGTCTCCCAAGTTTCC 807
                                                                                                                                                                                                                                                                                                                                                                                                          133 LeuGlyLysGlyIleAsnGlnAlaSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 GCCCAAAAATGTGCTTCAAATCCTGGAAAGGCAAGGGCTAGAGAGGTGATAAACCCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 TTGGACTC-CAATCAGATCACATTCATCCCCAATGAGATTTTTAAGGGACCTCCATCAAC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 LeuThrThrAsnGlnThrAlaArgValLeu---ValAlaGlyHisThrAspGluArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 PheAspPheAspSerAspGluIleLysProGln------
NIH-MGC http://mgc.nci.nih.gov/.
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 503)
                                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                                                                                         BE261626 503 bp mRNA linear EST 20-001-2601149316F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502299 5',
                                                                                                   Homo sapiens
                                                                                                                               human.
                                                                                                                                                   BE261626.1 GI:9133944
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10315 row: p column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnAspGluThrValLysAlaLeuAlaSerLysLeuProSer-----LeuValTyr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295
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Location/Qualifiers
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276 c 285 g 227 t
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/lab_host="DBHOB (phage-resistant)"
/note="organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4481142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_94"
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79.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 3 High quality sequence stop: 502.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                            LeuGlyGlu----
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140 AlaSerValGluIle
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                                                                                                                                                                                                                                                        61 AlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                          34 TACGTTCAAATCGGAGCCGCCGCCGCAGTCACCATGGGCCTCGGATACTACTTGTCGAAG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 HisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCys 23
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Fax: 81-559-81-6855
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Yata 1111, Mishima, Shizuoka 411, Japan
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                                                       LeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGln 139
                                                                                            GCGCGCACCCTCTACCAGGGT-----GTTCGCCGNGGAGCCCGTCTCTCGAAC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ykohara@lab.nig.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole animal"
/dev_stage="varied"
112 c 96 g 76 t
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/sex="hermaphrodite, male"
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/db_xref="taxon:6239"
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Seq primer: GTAAAACGACGGCCAGTG
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Fax: 864 656 4293
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/db_xref="taxon:4530"
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AQ954996 470 bp DNA linear GSS 27-JAN-nbeb0076M14f CUGI Rice BAC Library (ECORI) Oryza sativa genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                               Anotes "Wector: pBACINDIA'O; Site_1: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the hunid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Leaf"
/lab_host="E. coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pgp2n.pk007.o23 Normalized Chicken Pituitary/Hypothalamus/Pineal Library (pgp2n) Gallus gallus clone pgp2n.pk007.o23 5' similar to results pending, mRNA sequence.
BM491955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Townsend Hall, Newark, DE 19717,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Contact: Larry A. Cogburn
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Porter, T.E. and Cogburn, L.A.
ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
library, USDA/IFAFS Animal Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cogburn@udel.edu, www.chickest.udel.edu.
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                                                                                                      /note="Vector: pCMVSPORT6; Library made from pools of total RNA isolated from each tissue ages. Single pass sequencing 5'-end" 230 c 227 g 105 t 15 others
                                                                                                                                                                                                                                                                                              /clone="pgp2n.pk007.o23"
/clone_lib="Normalized Chicken
Pituitary/Hypothalamus/Pineal Library (pgp2n)"
                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
/strain="Commercial broiler chickens"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                  /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                     491 CCGGAGGGTGGCCGATTTAAGAAGGAG 517
                                                                                                           142 ValGluIleIleSerPheGlyGluGlu 150
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                                                                                                                                                                                   GluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSer 141
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